

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 14:29:20 ; Search time 39 Seconds

(without alignments)

2937.810 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRNGSSCDTVDQYQCFSE.....SPVRGLSFARSGGDNAECFA 444

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2294	98.3	467	Q9U27	Q9U27 aspergillus
2	2260	96.8	448	Q9J255	Q9J255 aspergillus
3	2259	96.8	467	Q93838	Q93838 aspergillus
4	2249	96.4	467	Q9HEQ0	Q9HEQ0 aspergillus
5	1610	69.0	465	Q9C171	Q9C171 aspergillus
6	1606.5	68.8	465	Q00092	Q00092 aspergillus
7	1605.5	68.8	442	Q8KZU5	Q8KZU5 aspergillus
8	1520	65.1	466	Q00100	Q00100 aspergillus
9	1496.5	64.1	466	Q0C096	Q0C096 aspergillus
10	1493	64.0	466	Q0C085	Q0C085 aspergillus
11	129.5	48.4	487	Q0C107	Q0C107 thielavia h
12	762.5	32.7	443	Q96VF5	Q96VF5 trameetes pu
13	752.5	32.2	439	Q96VH9	Q96VH9 pericophora
14	739.5	31.7	453	Q96V70	Q96V70 agrocyste pe
15	739	31.7	442	Q96VK9	Q96VK9 cf. ceripor
16	732	31.4	442	Q96VK8	Q96VK8 cf. ceripor

17	357	15.3	482	3	Q8X1W7	Q8X1W7 morascus an
18	355	15.2	469	3	Q9Y846	Q9Y846 kluyveromyc
19	302.5	13.0	442	3	Q74677	Q74677 pichia angu
20	300	12.9	463	3	Q60172	Q60172 schizosacch
21	225	9.6	451	11	Q35217	Q35217 ratiuss norv
22	216	9.3	467	5	Q9VW72	Q9VW72 drosophila
23	212	9.1	481	11	Q8VDRQ	Q8VDRQ mus musculu
24	210	9.0	481	11	Q922L6	Q922L6 mus musculu
25	209	9.0	449	13	Q92170	Q92170 gallus gai-
26	204	8.7	487	4	Q95172	Q95172 homo sapien
27	203	8.7	487	4	Q9UNW1	Q9UNW1 homo sapien
28	202	8.6	467	5	Q96421	Q96421 drosophila
29	201	8.6	487	4	Q9UGA3	Q9UGA3 homo sapien
30	185.5	7.9	464	13	Q90X11	Q90X11 fugu rubrip
31	185	7.9	453	5	Q96420	Q96420 drosophila
32	184	7.9	453	5	Q9W438	Q9W438 drosophila
33	176.5	7.6	487	10	Q941B2	Q941B2 arabidopsis
34	157	6.7	274	11	Q94JD5	Q94JD5 mus musculu
35	148	6.3	468	10	Q04509	Q04509 arabidopsis
36	147	6.3	210	5	Q8T312	Q8T312 drosophila
37	142	6.1	606	16	Q8G772	Q8G772 bifidobacte
38	137.5	5.9	198	3	Q9UTX1	Q9UTX1 schizosacch
39	137.5	5.9	374	11	Q9JMG5	Q9JMG5 mus musculu
40	137.5	5.9	416	11	Q8BP40	Q8BP40 mus musculu
41	136.5	5.8	38	11	Q90XG5	Q90XG5 mus musculu
42	132.5	5.7	1041	16	Q8EUZ5	Q8EUZ5 mycoplasma
43	128	5.5	480	11	Q8B212	Q8B212 mus musculu
44	127	5.4	480	11	Q8BHA9	Q8BHA9 mus musculu
45	120.5	5.2	413	16	Q8XBZ6	Q8XBZ6 escherichia

ALIGNMENTS

RESULT :

Q9U27 PRELIMINARY; PRT; 467 AA.
 ID Q9U27
 AC Q9U27
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Nyo-incsitol hexaphosphate phosphohydrolyase precursor
 (EC 3.1.3.8).
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 CX NCB:TaxID:5061;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Horgning W., Qi W., Jing X.;
 RT "PCR cloning and characterization of the phytase (phyA) gene of
 R. Aspergillus niger (China Strain)";
 RJ Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CR EMBL; AF218813; AAF25481.1; -
 DR HSSP; P34752; 11HP.
 DR InterPro; IPR000560; HisAc phosphatase.
 DR Pfam; PF00328; acid phosphatase 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolyase; Lyase; Signal.
 FT SIGNAL 1 19
 FT SIGNAL 19
 SQ SEQUENCE 467 AA; 51030 MW; F4300A8F165EBF92 CRC64;

Query Match 98.3%; Score 2294; DB 3; Length 467;

Best Local Similarity 97.5%; Pred. No. 1.9e-167;

Matches 433; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASRNGSSCDTVDQYQCFSETHLWQYAFPFSSLANESVISPEVPACGRTVFAQVLSRHG 60

24 ASRNGSTCDTVDQYQCFSETHLWQYAFPFSSLANESVISPDVFACTVFAQVLSRHG 83

61 ARYPTDSKKYKYSALIREIQONATTFGKAFATLTYNSLCADDLTFGQELVNSGIKF 120

```

Db 84 ARYPTDSKGGKYSALIEIQONATTGCKYAPLKTNYSLGADDLTPGCEQLVNSGKIF 143
QY 121 YORYESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 180
Db 144 YORYESLTRNIIPIFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 240
Db 204 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 300
Db 264 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 420
Db 384 TTQVNIOTQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
ID Q8J255 PRELIMINARY; PRT: 448 AA.
AC Q8J255
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phytase (Fragment).
GN PHVA.
OS Aspergillus ficuum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Zhu J., Sun J., Wu Z., Wang L., Chen G., Jiang H., Li M.;
RI Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF517344; AAK10115.1; -.
FT NON-TER
SQ
SEQUENCE 448 AA; 49260 MW; 05547F9712FF7BAA CRC64;

Query Match 96.8%; Score 2260; DB 3; Length 448;
Best Local Similarity 95.5%; Pred. No. 7.4e-165;
Matches 424; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 ASRNCSSCDTVDOGYCCFSETSHLMGOYAPFFSLANESVISPVPAGCRVTFQAVLSRHG 60
Db 5 ASRNCSSCDTVDOGYCCFSETSHLMGOYAPFFSLANESVISPVPAGCRVTFQAVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEIQONATTGCKYAFPLKTNYSLGADDLTPGCEQLVNSGKIF 120
Db 65 ARYPTDSKGGKYSALIEIQONATTGCKYAFPLKTNYSLGADDLTPGCEQLVNSGKIF 124
QY 121 YORYESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 180
Db 125 YORYESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 184
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 240
Db 185 STSNKTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 244
QY 241 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 300
Db 245 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 304
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360

```

```

Db 305 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLSS 364
QY 361 TTVENITQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 420
Db 365 TTAENITQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 424
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Db 425 CTRDSFVRGLSFARSGGDWAECEFA 448

RESULT 3
ID Q93838 PRELIMINARY; PRT: 467 AA.
AC Q93838
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytase.
GN PHVA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RI "Phytase having high-affinity for phytic acid."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB022700; BAA74433.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; HisAc_phosphatase.
DR Pfam; PF00328; acid_phosphat_1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ
SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;

Query Match 96.8%; Score 2259; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 9.4e-165;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNCSSCDTVDOGYCCFSETSHLMGOYAPFFSLANESVISPVPAGCRVTFQAVLSRHG 60
Db 24 ASRNCSSCDTVDOGYCCFSETSHLMGOYAPFFSLANESVISPVPAGCRVTFQAVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEIQONATTGCKYAFPLKTNYSLGADDLTPGCEQLVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEIQONATTGCKYAFPLKTNYSLGADDLTPGCEQLVNSGKIF 143
QY 121 YORYESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 160
Db 144 YORYESLTRNIVPFRSSGSRVIAKGFIEGQSTKLKDPRAQPGOSSPKIDVWVSEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 240
Db 204 STSNKTLDPGCTCTVFEDSELADVEANFTATVPFSIRORLENDLSGVTCTDEVTYLMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 300
Db 264 CSFDTISTSTVDTKLSPFCDLFTHEMINVDYLSLKYYHGHGAGNPLGPTQGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLSS 383
QY 361 TTVENITQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 420
Db 384 TTAENITQTDGFSSAWTVPFASRLYVENMQCAEQEPLVRVLVNDRVVPLHGPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444

```


RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
 RT "Gene cloning, purification, and characterization of a heat-stable
 RL phytase from the fungus *Aspergillus fumigatus*.";
 RL Appl. Environ. Microbiol. 63:1696-1700(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
 CC A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO
 CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
 CC CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE
 CC INITIAL ENZYMIC ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC EMBL: U59804; AAB96872.1; --
 DR HSP; P34752; 1:HP.
 DR InterPro: IPR000560; HisAc_phspstse.
 DR Pfam: PF00328; acid_phosphat_1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 465
 FT ACT_SITE 81 81
 FT ACT_SITE 82 82
 FT ACT_SITE 359 359
 FT DISULFID 30 39
 FT DISULFID 70 412
 FT DISULFID 213 463
 FT DISULFID 262 280
 FT DISULFID 434 442
 FT CARBOHYD 104 104
 FT CARBOHYD 119 119
 FT CARBOHYD 205 205
 FT CARBOHYD 228 228
 FT CARBOHYD 337 337
 FT CARBOHYD 350 350
 FT CARBOHYD 374 374
 SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;
 Query Match 68.8%; Score 1606.5; DB 3; Length 465;
 Best Local Similarity 66.4%; Pred. No. 9.4e-115;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
 QY 1 ASRQSCDVTDOGYQCFSETSLHWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 60
 DB 23 SSAGSKCDTVDLGYQCSPTATSLHWQYSPFFSLEDELSVSKLPKOCRITLVQVLSRHG 82
 QY 62 ARYPTDSKGYKYSALIEECCQNAITFDGKYAEKTYNYSIGADDLTPGQELVNSGTFK 120
 DB 83 ARYPTSSKKYKLVTAIQANATDFKGFAPLKTNYTLGADDLTPGEOQLVNSGIFK 142
 QY 121 YQYESLTRNIVPFISSGSSRVIASGKGFIEGQSTKLKDPRAQGGSSPKIDVISEA 180
 DB 143 YQYKALARSVVPFIASGSDRVIASGKGFIEGQCAKLADPGA-TNRAAPAIISVIIPE 201
 QY 181 SSSNNTLDPGCTVFEDSELADTVENATFVPSIRORLENDLSGVTLTCTETVLMGX 240
 DB 202 ETPNNTLDHGVCITKFEASQSGDEVAANFTALFAPDIRAEAKHLPGVTLTDEDVVS 261
 QY 241 CSFTITSTSTVDTKLSPPFCOLFHDENINYDYCSLKKYVGHGAGNPGPTQGVYANEL 300
 DB 262 CSFTVARTSDASQSLSPFCOLFTHNEWKYNVLSLGYGYGAGNPLGPAQGIQFTNEL 321
 QY 301 IARLTHSPVDDTSSNHTLDSSPATFPNSTLYADFSHNGIISILFALGLYNGTKPLST 360
 DB 322 IARLTRSPVQDHTSTNSTLVSNPATFPNLATMYVDFSHDMSVSPFALGLYNGTEPLSR 381
 QY 361 TTVENITCTDGFSSAMTVPFASLYVEMMOCAEQEPLVRVLVNDRVVPLHCCPVDALGR 420
 DB 382 TSVESAKELDGYASWSVVPFGARAYFETMOCKSEKPEPLVRALINDRVVPLHCCVDK 441

QY 421 CTRDSFVRGLSPARSGGDWAECPA 444
 DB 442 CKLNDVFKGLSWARSGGNWGECS 455
 RESULT 7
 Q8WZJ5
 ID Q8WZJ5 PRELIMINARY; PRT; 442 AA.
 AC Q8WZJ5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase (EC 3.1.3.8; precursor (Fragment)).
 GN PHIA3.
 CS *Aspergillus fumigatus* (Sartorya fumigata).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCCTCC AF93024;
 RA Zhang G.;
 RT "Cloning of phytase gene from *Aspergillus fumigatus* and its expression
 RL in *Pichia pastoris*.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ419776; CAD12029.1; --
 DR InterPro: IPR000560; HisAc_phspstse.
 DR Pfam: PF00328; acid_phosphat_1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Signal; Hydrolase.
 FT NCN_TER 1 1
 FT SIGNAL <1 3 POTENTIAL.
 FT CHAIN 4 442 PHYTASE.
 SQ SEQUENCE 442 AA; 48485 MW; 3FDBAC656A268514 CRC64;
 Query Match 68.8%; Score 1605.5; DB 3; Length 442;
 Best Local Similarity 66.6%; Pred. No. 1e-114;
 Matches 295; Conservative 58; Mismatches 89; Indels 1; Gaps 1;
 QY 2 SRNQSCDVTDOGYQCFSETSLHWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHGA 61
 DB 1 SAGSKCDTVDLGYQCSPTATSLHWQYSPFFSLEDELSVSKLPKOCRITLVQVLSRHGA 60
 QY 62 RYPTDSKGYKYSALIEECCQNAITFDGKYAPLKTNYNYSIGADDLTPGQELVNSGIFK 121
 DB 62 RYPTSSKKYKLVTAIQANATDFKGFAPLKTNYTLGADDLTPGEOQLVNSGIFK 120
 QY 122 QRYESLTRNIVPFISSGSSRVIASGKGFIEGQSTKLKDPRAQGGSSPKIDVISEAS 181
 DB 121 QRYKALARSVVPFIASGSDRVIASGKGFIEGQCAKLADPGA-TNRAAPAIISVIIPE 179
 QY 192 SSSNNTLDPGCTVFEDSELADTVENATFVPSIRORLENDLSGVTLTCTETVLMDC 241
 DB 180 TTNNTLDHGVCITKFEASQSGDEVAANFTALFAPDIRAEAKHLPGVTLTDEDVVS 239
 QY 242 SFTTSTSTVDTKLSPPFCOLFHDENINYDYLSLKKYVGHGAGNPLGPTQGVYANEL 301
 DB 240 SFTVARTSDASQSLSPFCOLFTHNEWKYNVLSLGYGYGAGNPLGPAQGIQFTNEL 299
 QY 302 IARLTHSPVDDTSSNHTLDSSPATFPNSTLYADFSHNGIISILFALGLYNGTKPLST 361
 DB 300 IARLTRSPVQDHTSTNSTLVSNPATFPNLATMYVDFSHDMSVSPFALGLYNGTEPLSR 359
 QY 362 TTVENITCTDGFSSAMTVPFASLYVEMMOCAEQEPLVRVLVNDRVVPLHCCPVDALGR 421
 DB 360 TSVESAKELDGYASWSVVPFGARAYFETMOCKSEKPEPLVRALINDRVVPLHCCVDK 419
 QY 422 TRDSTFVRGLSPARSGGDWAECPA 444
 DB 420 KLNDFVFKGLSWARSGGNWGECS 442

RESULT 8

```

ID O00100 PRELIMINARY; PRT; 466 AA.
AC O00100;
DT 01-JUL-1997 (TREMBlrel. 04, Created);
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE 3-phosphate precursor (EC 3.1.3.8) (MYO-inositol-hexaphosphate 3-phosphohydrolase) (3 phytase) (MYO-inositol hexakisphosphate phosphohydrolase);
DE Aspergillus terreus;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=33178;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 116.46;
RA Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B., Broger C., van Loon A.P.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL; U60412; AAB58465.1; -.
DR HSP; P34752; 1IHP.
DR InterPro; IPR000560; HisAc_pshptase.
DR Pfam; PF00328; acid phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 466 3-PHYTASE.
FT ACT_SITE 82 82 REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY).
FT ACT_SITE 83 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 71 414 BY SIMILARITY.
FT DISULFID 215 465 BY SIMILARITY.
FT DISULFID 264 282 BY SIMILARITY.
FT DISULFID 436 444 BY SIMILARITY.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 466 AA; 51055 MW; F2AECACAF7C22C4 CRC64;

Query Match 65.1%; Score 1520; DB 3; Length 466;
Best Local Similarity 63.4%; Pred. No. 4e-108;
Matches 279; Conservative 65; Mismatches 96; Indels 0; Gaps 0;

QY 4 NOSSCDTVDDGYQCFSSTSHLWGQYAPFFSLANESVTSPEVPAGCRVTFQAQVSRRGARY 63
D 27 NNSDCTSVDRGYQCFFELSHKMGWLYAPFSLQDESPPFLDVPDCHITFFQVQLARHGARS 86
QY 64 PTDSKGKYSALIEIQONATTFDCKYAFKTYNYSLGADLTFFGCEGLVNSGKIFQYOR 123
D 87 PTDSKTKAYAAATAAIQKNATAJPGKAFKLSYNSMGSENLPFGNQLQDLGACFYRR 146
QY 124 YESLTRNIVPTIRSSGSRVIAASKKKEGFSQTKLKDPRAPQCGSSPKIDVVISASSS 193
D 147 YDTU:TRHINPVRADSRVHSEAKKEVFGFNARQGDPRANPHQSPRVDDVWIPGATAY 206
QY 184 NNTLDPGCTVFDESELDATVEANFTATFVPSIRORLENDLSGVTLTDEVTYLMDCWCF 243

```

```

DB 207 NNTLEHSICTAFEAESTVGDAAADNFTAVFAPAIKRLEADLPGLVQLSADVDWNLXAMCFF 266
QY 244 DTISTSTVDTKLSPFCDLFTHEWMINVDYQSLKKYGHGAGNFPPTQGVGYANELLAR 303
D 267 ETVSILTDDAHTLSPFCDLFTAAEWTQYNLLSLDKYGYGGNPLGPGVQGVGMANEJLAR 326
QY 304 LTHSPVHDDTSSNHTLSSPATFNLSTLYADFSDHNGI:SLFALGLYNTKPKLSTTTV 363
D 327 LTRSPVHDDTTCVNNLTLDANPATFNLATLYADFSDHNSLVSIWALGLYNTKPKLSQTTV 386
QY 364 ENITOTQCFSSAWTPFASRLYVNMVQCBQEBLVRVLVNDRVVPVHGCPVCAJLGRCTR 423
D 397 EDITRTDGYAAAWTPFAARAYIEMMQCRABKQLVRVLVNDRVVPLHGCAVDNLGRCKR 446
QY 424 DSFVRGLSFAIRSGSDWAECP 443
D 447 DDFVEGLSFARAGGNWAECP 466

RESULT 9
O00096 PRELIMINARY; PRT; 466 AA.
ID O00096;
AC O00096;
DT 01-JUL-1997 (TREMBlrel. 04, Created);
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE Phytase (EC 3.1.3.8);
DE Talaromyces thermophilus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Talaromyces.
OX NCBI_TaxID=28565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716;
RA Pasamontes L., Haiker M., Henriquez Huecas M., Mitchell D.B., van Loon A.P.;
RT "Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus.";
RL Biochim Biophys Acta 1353:217-223 (1997).
DR EMBL; U59402; AAB96873.1; -.
DR HSP; P34752; 1IHP.
DR InterPro; IPR000560; HisAc_pshptase.
DR Pfam; PF00328; acid phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase.
SQ SEQUENCE 466 AA; 51450 MW; FC4575B521A5C929 CRC64;

Query Match 64.1%; Score 1496.5; DB 3; Length 466;
Best Local Similarity 62.2%; Pred. No. 2.5e-106;
Matches 278; Conservative 58; Mismatches 106; Indels 5; Gaps 2;

QY 2 SRN----OSSCDTVDDGYQCFSSTSHLWGQYAPFFSLANESVTSPEVPAGCRVTFQAQVLS 57
D 18 SRNPHVDSHSNTVEGGYQCRPEISHSWGQYSPFFSLADQSEISPDVPQNCKITFVQLLS 77
QY 58 HGARYPTDSKGKYSALIEIQONATTFDCKYAFKTYNYSLGADLTFFGCEGLVNSG 117
D 78 HGARYPTDSKTKAYAAATAAIQKNATAJPGKAFKLSYNSMGSENLPFGNQLQDLGACFYRR 137
QY 118 IKFYORYESLTRNIVPTIRSSGSRVIAASKKKEGFSQTKLKDPRAPQCGSSPKIDVVI 177
D 138 IKFYNHYSKLARNAVPFVRCSSDRVIAAGRLFIEGFSQAKVLDPHSKDKCAPTINVII 197
QY 178 SEASSNNTLDPGCTVFDESELDATVEANFTATFVPSIRORLENDLSGVTLTDEVTYL 237
D 198 EGGPSYNTLDTGSCVPFEDSSGCHDAQEKFAKQAPALIEKIKDHLPGVLDVSDVPY 257
QY 238 NDCMSFDITISTSTVDTKLSPFCDLFTHEWMINVDYQSLKKYGHGAGNPLGPTQGVGYA 297
D 258 MDLCPEFTIARNHTDTLSPEFCA:STOBEWQAYDYQSLGKYGNGGNPLGPAQGVGFV 316
QY 298 NELIARLTHSPVHDDTSSNHTLSSPATFNLSTLYADFSDHNGI:SLFALGLYNTKPK 357

```

Best Local Similarity 52.3%; Pred.No. 4.7e-16;
Matches 273; Conservative 69; Mismatches 97; Indels 0; Caps 0;

QY	6	SSCDTVDOOGCCFSETSHWGQYAFPFESANESVISREVPAGCRVTFAQVLSRHGARYPT	65
DB	29	SCDSVDHGVCQCPFESHKXGVLGYAFSLQDESFFPLDVPEDCHITFVQVLARAGARSPT	88
QY	66	DSKOKKYSALIEIQNAWTFPGKYAFIKTNYNSLGADLTPPGEQLVNSG-KFYQRYE	125
DB	89	HSKTKAYAAITAIIOKSATAFGKYAFICSNYSLDSELTPPFCRNO.RDLGQAFVERYN	148

[illegible]

HSSP; P34752; LHF.
InterPro; IPR000560; HisAc_phsphtse.


```

DR Pfam: PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; H-S_ACID_PHOSPHAT_2; 1.
DR KX Hydrolase; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 453 PHYTASE.
SQ SEQUENCE 453 AA; 4933; MW; D62FIAEFA10915ED CRC64;

Query Match 31.7%; Score 739.5; DB 3; Length 453;
Best Local Similarity 36.8%; Pred. No. 2,5e-48;
Matches 161; Conservative 83; Mismatches 152; Indels 41; Gaps 11.

QY 25 MCQYAPFSLANESVIGPEVPAGCVRVTFACVLGRHGRARPTDSKGGKYGAL-EEIQGNAT 94
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
39 WAAATPYTPV--QAYTP--PKCKKITQVNIIRHGARGFTSGAGTRIOAAVKKLQSAXT 94
QY 65 TFGGKVAFLKTYNYSLGADDTLPFGDELVNSGIKFYQRYESL-TRNI-VPIRSSSSSRV 143
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95 YTDPLDLFTNYTYTLGHDDLVPFGALQSSQAGEE:FORVSF-VSKENLPFYRASSNRV 154
QY 144 TASGKKFTIEGFSQTKLKDPRACQGOSSPKIDVW:SEASSNNTLDPGTCTVFEDESLAT 203
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155 VDSATNWTEGFS-ASHHVLNPILFVILSE--SLNDTLDAMC---PNAGSSDP 202
QY 204 VEANFTATFVPSIRGLNDLSGVTLTCTEVTYLMQMCSEDTISTGTVTKLSPFCDLFT 263
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 QTGHTSIYGTPIANRLNQCPAGNITAADVSNLILFCAFEIVKETP---SPPNLF 258
QY 264 HDEWNIYDLOSLLKXYGHGAGNPLGPTQGVGYANEL:ARLTHSPVHDDTSSNHTLDSGP 323
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
259 PEEFAQFEGYGLGOKFYGTGTGVQGP:GPGVGVGYINEL:ARLTMPVRDNTQTNRT:CSSP 318
QY 324 A7PLNSTLYADFSRONGIISIFALG:YNGTKPLSTTTVENITCTDGTSSAMTVPFASR 383
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
319 LTFPLRSIYADLSHNOX:ILFSA:GLFNQSSPLD-PSFPHKRT--WVTSRLTPPSAR 375
QY 364 JYVEMVQCOAE-----DEPLVRVANDRVFLHGCVPVDALGRCTRGSFVR 428
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
376 MVTEALLQCRGTGSGGPSRINRNGNVQTFVRLVNDALQLKFCGQDMSLTLEAFVE 435
QY 429 GLSPARSG--GDWAECP 443
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
436 SQKYAREDDGQDFEACP 452

RESULT 15
Q96VK9 PRELIMINARY; PRT; 442 AA.
ID Q96VK9 AC Q36VK9
1D Q96VK9 AC Q36VK9
CT 01-DEC-2001 (TrEMBLrel. 19, Created)
Dt 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Dt 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phytase precursor (EC 3.1.1.3,26).
GV PHYAL.
CS cf. Ceriporia sp. CBS 100231.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Achyloporales; Ceriporia.
CX NCBI_TaxID=154783;
11.
RN SEQUENCE FROM N.A.
RP STRA:NCBS 100231.
RC Jassen S.F., Breinholt J., Ostergaard P.R., Bruggen R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RA "Expression cloning and characterization of five novel phytases from
RT four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, cf.
RT Ceriporia and Trametes pubescens."
RJ Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
RJ EMBL: AJ110698; CAC48163.1;
DR Inter-Pro: IPR000560; HisAc_phosphatse.
DR Pfam: PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; H-S_ACID_PHOSPHAT_2; 1.
DR KX Hydrolase; Signal.

```

01-DEC-2001 (TREMBLrel_19). Created!
DT 01-DEC-2001 (TREMBLrel_19). Last sequence update!
CT 6-MAR-2003 (TREMBLrel_23). Last annotation update;
DE Phytase precursor (EC 3.1.3.26);
DM PHYA.
GN GN
CS cf. Ceriporia sp. CBS 100231.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Ceriporia.
CX NCBI_TaxID=154783;
RX 11.
SEQUENCE FROM N.A.
RP STRAIN=CBS 100231;
RA Jassen S.F., Breinholt J., Ostergaard P.R., Bruggen R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RT "Expression cloning and characterization of five novel phytases from
RT four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, cf.
RT Ceriporia and Trametes pubescens";
EL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ310698; CAC48163.1; ...
DR InterPro: IPR000560; HisAc_pnsphtse.
DR Pfam: PF03328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; H-S_Ac-D_PHOSPHAT_2; 1.
KW Hydrolase; Signal.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 14:26:15 ; Search time 17 Seconds
(without alignment)

1228.227 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRNSQSDTVQGIQCFSE.....SFVCG:SPARSGGDWAECA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	467	PHYA_ASPNG	P34752 aspergillus
2	2290	98.1	467	PHYA_ASPNG	P34753 aspergillus
3	1532.5	65.7	463	PHYB_ENENI	Q00093 emeritella
4	385	16.5	467	PPA3_YEAST	P24031 saccharomyc
5	385	16.5	467	PPA5_YEAST	PC5635 saccharomyc
6	368	15.8	468	PPAD_YEAST	P52290 saccharomyc
7	352	15.1	467	PPAB_YEAST	P35842 saccharomyc
8	352	15.1	467	PPAC_YEAST	P38693 saccharomyc
9	351	15.0	469	PPA5_KLJLA	P52289 kluyveromyc
10	339.5	14.5	479	PHYB_ASPNG	P34754 aspergillus
11	336.5	14.4	479	PHYB_ASPNG	P34755 aspergillus
12	327	14.0	468	PPA1_PICPA	P52292 pichia past
13	296.5	12.7	453	PPA1_SCHPO	P08091 schizosacch
14	284	12.2	463	PPA2_SCHPO	Q01682 schizosacch
15	119.5	5.1	413	AGP_EECFI	P19926 escherichia
16	115	4.9	590	PEPP_BORBU	O51264 borrelia bu
17	109.5	4.7	413	AGP_SALTY	O33921 salmonella
18	107	4.6	2314	PTP2_HUMAN	P23471 homo sapien
19	106	4.5	507	RRPE_CDOVO	P36940 canine dist
20	106	4.5	755	PPAX_CAEEL	Q09549 caenorhabdi
21	105.5	4.5	422	PPAY_CAEEL	Q10944 caenorhabdi
22	104.5	4.5	1254	UBPC_YEAST	P39538 saccharomyc
23	104	4.5	504	CP12_RAT	P05183 rattus norv
24	104	4.5	1306	MSB2_YEAST	P32334 saccharomyc
25	102	4.4	927	CC15_SCHPO	Q09822 schizosacch
26	101.5	4.3	421	PPAL_MOUSE	P24638 mus musculu
27	101	4.3	667	Y431_HUMAN	Q43313 homo sapien
28	101	4.3	677	NRG1_XENLA	O93383 xenopus lae
29	100.5	4.3	936	PMPT_CHJPN	Q92898 chlamydia p
30	99.5	4.3	658	LITB_STRPN	P59205 streptococc
31	99	4.2	567	CH13_CANAL	P40354 candida alb
32	98.5	4.2	423	PPAL_RAT	P20611 rattus norv
33	98	4.2	423	PPAL_HUMAN	P11117 homo sapien

ALIGNMENTS

```

RESULT 1
PHYA_ASPNG
ID PHYA_ASPNG STANDARD; PRT: 467 AA.
AC P34752;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
DE 3-phosphorylase A; (3 phytase A) (Myo-inositol hexakisphosphate
DE 3-phosphohydrolase A).
GN PHYA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=93252284; PubMed=8387447;
RA van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
RA Gouka R.J., Snykterbuyk M.B.G., Luiten R.G.M., van Paridon P.A.,
RA Sellen G.C.X., Veenstra A.E., van Gorcom R.F.M.,
RA van den Hondel C.A.M.J.C.;
RA "Cloning, characterization and overexpression of the phytase-encoding
RT gene (phyA) of Aspergillus niger.";
RT Gene 127:87-94(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mullaney E.J.;
RA Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 24-464.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=93249451; PubMed=8387289;
RA Ullah A.H.J., Cummings B.J., Dischinger H.C. Jr.;
RA "Aspergillus ficuum phytase: complete primary structure elucidation
RT by chemical sequencing.";
RN Biochem. Biophys. Res. Commun. 192:747-753(1993).
RN [4]
RP SEQUENCE OF 71-93.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=91298982; PubMed=1648914;
RA Ullah A.H.J., Cummings B.J., Dischinger H.C. Jr.;
RA "Cyclohexanediol modification of arginine at the active site of
RT Aspergillus ficuum phytase.";
RN Biochem. Biophys. Res. Commun. 178:45-53(1991).
RN [5]
RP CHARACTERIZATION, AND PARTIAL SEQUENCE.
RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=89160685; PubMed=2852807;
RA Ullah A.H.J.;
RA "Aspergillus ficuum phytase: partial primary structure, substrate
RT selectivity, and kinetic characterization.";
RN Prep. Biochem. 18:459-471(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

```

```

34 98 4.2 526 1 CLOS_CLOHI
35 98 4.2 1374 1 YODI_SCHPO
36 97.5 4.2 596 1 MPFI_SCHPO
37 97 4.2 822 1 YJFI_YEAST
38 96.5 4.1 504 1 C34_MOUSE
39 96.5 4.1 702 1 LYTS_STR6
40 96.3 4.1 1419 1 ALAI_CANAL
41 96 4.1 2258 1 PAS_FIG
42 96 4.1 3137 1 CA36_CHCK
43 95.5 4.1 1328 1 YMT5_YEAST
44 95 4.1 3010 1 POLG_HCVJT
45 94.5 4.0 636 1 YNR6_YEAST

```

```

P09570 cistricidin
Q09884 schizosacch
P06652 schizosacch
P47046 saccharomyc
Q9jma7 mus musculu
P59206 streptococc
O13168 candida alb
Q99191 sus. scrofa
P15989 gallus gall
O04214 saccharomyc
Q00269 h genome po
P53882 saccharomyc

```

RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUJM;
 RX MEDLINE=97307250; PubMed=9764457;
 RA Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell C.,
 RA van Loon A.P.;
 RI "Crystal structure of phytase from *Aspergillus ficuum* at 2.5-A
 RI resolution.";
 RJ Nat. Struct. Biol. 4:185-190(1997).
 CC !- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC !- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
 CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
 CC !- BIOTECHNOLOGY: Is used as a food and feed additive. It can
 CC facilitate the degradation of phytin in soybean and other seeds
 CC used as food for monogastric animals. Sold by Novo Nordisk under
 CC the name Phytase Novo.
 CC !- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z16414; CAA78904.1; -
 CC EMBL; M94550; AAA32705.1; -
 CC PIR; JN0656; CNO656.
 CC PDB; 1IHP; 18-MAR-98.
 DR InterPro; IPR000560; HisAc phosphatase.
 DR Pfam; PF00328; acid phosphatase.
 DR PROSITE; PS00616; HIS-ACID-PHOSPHAT-1; 1.
 DR PROSITE; PS00778; HIS-ACID-PHOSPHAT-2; 2.
 KW Hydrolase; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 467 3-PHYTASE A.
 FT ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 31 40
 FT DISULFID 71 44
 FT DISULFID 25 465
 FT DISULFID 264 282
 FT DISULFID 436 444
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .)
 FT STRAND 32 33
 FT TURN 34 36
 FT STRAND 37 38
 FT TURN 40 42
 FT HELIX 42 45
 FT TURN 46 47
 FT HELIX 49 51
 FT STRAND 53 53
 FT STRAND 55 55
 FT HELIX 58 60
 FT TURN 69 70
 FT STRAND 71 81
 FT STRAND 85 85
 FT HELIX 89 105
 FT HELIX 111 118
 FT STRAND 128 128
 FT HELIX 130 146
 FT TURN 147 147
 FT HELIX 148 151
 FT TURN 152 153

FT STRAND 157 161
 FT HELIX 164 182
 FT TURN 183 183
 FT TURN 185 186
 FT TURN 189 190
 FT STRAND 196 200
 FT TURN 204 205
 FT TURN 209 210
 FT HELIX 216 220
 FT HELIX 223 233
 FT TURN 234 235
 FT HELIX 236 246
 FT TURN 248 249
 FT HELIX 254 269
 FT TURN 270 270
 FT HELIX 280 284
 FT HELIX 287 304
 FT TURN 305 305
 FT TURN 307 308
 FT TURN 310 312
 FT HELIX 313 316
 FT HELIX 317 328
 FT TURN 329 329
 FT HELIX 340 343
 FT TURN 346 348
 FT STRAND 355 360
 FT HELIX 362 372
 FT TURN 372 377
 FT TURN 389 394
 FT HELIX 397 400
 FT STRAND 403 403
 FT TURN 404 404
 FT STRAND 406 414
 FT TURN 421 426
 FT TURN 427 428
 FT STRAND 429 430
 FT TURN 440 441
 FT STRAND 444 445
 FT HELIX 446 452
 FT HELIX 454 457
 FT TURN 458 461
 FT HELIX 462 465
 FT TURN 466 467
 SQ SEQUENCE 467 AA; 51086 MW; 88FE9F3584341D6D CRC64;
 Query Watch 100.0%; Score 2334; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 5.4e-169; Indels 0; Gaps 0;
 Matches 444; Conservative 0; Mismatches 0;
 QY 1 ASRNQSSCTVQGYQCFSETSH:MGQYAPFFESLANESVISPEVPACRVTFAOVLSRHG 60
 DB 24 ASRNQSSCTVQGYQCFSETSH:MGQYAPFFESLANESVISPEVPACRVTFAOVLSRHG 83
 QY 61 ARYPTESKGYKYSALIEELIQONATTFOGYAPLTKYKSLGADDLTFEGECLVNSGKIF 120
 DB 84 ARYPTESKGYKYSALIEELIQONATTFOGYAPLTKYKSLGADDLTFEGECLVNSGKIF 143
 QY 121 YQRYESLTRNIVPFRSSSSSRVSIASGKKF:EGFQSTKLKDPRAQPGQSSPKIDWVISEA 180
 DB 144 YQRYESLTRNIVPFRSSSSSRVSIASGKKF:EGFQSTKLKDPRAQPGQSSPKIDWVISEA 203
 QY 181 SSSNNTLDFGCTTFPDSSELADTVANPTATFVPSIRQRIENDLSGVTLTDTTEVTYMDM 240
 DB 204 SSSNNTLDFGCTTFPDSSELADTVANPTATFVPSIRQRIENDLSGVTLTDTTEVTYMDM 263
 QY 241 CSFDTISTSTVDTKLSRFDCLPTHDEWINVDYLOS:KKYVGHGAGNP:GFTQGVGANEL 300
 DB 264 CSFDTISTSTVDTKLSRFDCLPTHDEWINVDYLOS:KKYVGHGAGNP:GFTQGVGANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383

QY 361 TTVENITOTDGFSSANTVPASRLVYVEMQCAEQEPLRVLYVNDRVLPVHGGCPVDALGR 420
 DB 384 TTVENITOTDGFSSANTVPASRLVYVEMQCAEQEPLRVLYVNDRVLPVHGGCPVDALGR 443

QY 421 CTRDSFVRGLSFARSGGDMACFA 444

DB 444 CTRDSFVRGLSFARSGGDMACFA 467

RESULT 2

PHYA ASPAW STANDARD; PRT; 457 AA.
 AC P34753; 1994 (Rel. 28, Created:
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
 DE 3-phosphohydrolase A) (3 phytase A) (Myo-inositol-hexakisphosphate
 DE phosphohydrolase A).
 GN PHYA OR PHY.
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Euctariales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
 CX NCBI_TaxID=165351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRAIN=AJ00243;
 RX MEDLINE=9404796; PubMed=8224894;
 RA Piddington C.S., Houston C.S., Palohelmo M.T., Cantrell M.A.,
 RA Mettinen-Oinonen A., Nevalainen H., Rambosk J.A.;
 RT "The cloning and sequencing of the genes encoding phytase (phy) and
 RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 RT awamori";
 RL Gene 133:55-62(1993).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = ID-
 CC MYO-INOSITOL 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: J02421; AAA16898.1; ..
 DR PIR: JN0889; JN0889.
 DR HSP: P34752; 11HP.
 DR InterPro: IPR000560; HisAc_phsphtase.
 DR Pfam: PF0328; acid_phsphtat; 1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal..
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAR 24 467 3-PHYTASE A.
 FT ACT SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 31 40 BY SIMILARITY.
 FT DISULFID 7 414 BY SIMILARITY.
 FT DISULFID 215 465 BY SIMILARITY.
 FT DISULFID 264 282 BY SIMILARITY.
 FT DISULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBCHVD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBCHVD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SC SEQUENCE 467 AA; 51275 MW; 118E928A5D7EC661 CSC64;

Query Match 98.1%; Score 2290; DB 1; Length 467;
 Best Local Similarity 97.3%; Pred. No. 110-165;
 Matches 432; Conservative 8; Mismatches 4; Indels C; Gaps 0;

QY 1 ASRNQSCDTVDQYQCFSETSHLWQVAPFSLANESVSPVYPAGCRVTFAQVLSRHG 60
 DB 24 ASRNQSCDTVDQYQCFSETSHLWQVAPFSLANESVSPVYPAGCRVTFAQVLSRHG 83
 QY 6: ARYFTDSKKKYSALIEIQONATTECKYAPLTYNYSACDCLTPGEGELVNSGKF 120
 DB 34 ARYFTDSKKKYSALIEIQONATTECKYAPLTYNYSACDCLTPGEGELVNSGKF 143
 QY 121 YCRYESLTRNVPFTRSSGSRVVIASGKKFIEGQSTKDKPRACPGQSSPKIDWVISEA 180
 DB 144 YCRYESLTRNVPFTRSSGSRVVIASGKKFIEGQSTKDKPRACPGQSSPKIDWVISEA 203
 QY 181 SSSNNTLDPGTCTVPEDSELADTVEANFTATFVPSIRQRLNDLGGVTLTDTTEVTYMDM 240
 DB 204 SSSNNTLDPGTCTVPEDSELADTVEANFTATFVPSIRQRLNDLGGVTLTDTTEVTYMDM 263
 QY 241 CSFDTISTVDIKLSPFCDLFTHDEWNYDVLQSLKKYVGHGAGNPLGPTGGVYANEL 300
 DB 264 CSFDTISTVDIKLSPFCDLFTHDEWNYDVLQSLKKYVGHGAGNPLGPTGGVYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSPPATFPLNSTJYADFSHDNGIISILFALGLYNGTKP-ST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSPPATFPLNSTJYADFSHDNGIISILFALGLYNGTKP-ST 363
 QY 361 TTVENITOTDGFSSANTVPASRLVYVEMQCAEQEPLRVLYVNDRVLPVHGGCPVDALGR 420
 DB 384 TTVENITOTDGFSSANTVPASRLVYVEMQCAEQEPLRVLYVNDRVLPVHGGCPVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDMACFA 444
 DB 444 CTRDSFVRGLSFARSGGDMACFA 467

RESULT 3

PHYB EMENI STANDARD; PRT; 463 AA.
 AC OCC093;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
 DE 3-phosphohydrolase B) (3 phytase B) (Myo-inositol-hexakisphosphate
 DE phosphohydrolase B).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Euctariales; Trichocomaceae; Emericella.
 CX NCBI_TaxID=162425;
 RE [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98007872; PubMed=9349716;
 RA Passantes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
 RA van Loon A.P.;
 RT "Cloning of the phytases from Emericella nidulans and the
 RT thermophilic fungus Talaromyces thermophilus";
 RL Biochim. Biophys. Acta 1353:217-223(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = ID-
 CC MYO-INOSITOL 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way


```

102 FNSGLFNDYFFIRDDDELEMTTFANSDVLPYTGEMAKHAREFLACYGYVE 161
130 NVVPF-IRSSGSRVSIAGKKFIEGPOSTKJOPRAQPGSSFKIDVSEASSNNTLD 188
162 NQTSFPFIAASSRVRHDTAQYFDG-----LGD-----QFN-SLQTVSEAMGAGANTLS 210
189 PGCTVFEDSELADTVEANTATATVPVSIORJENLDSGLTDTTEVTLMDMCSFDTIS 246
211 AGNACPGWDEADNDILCKYDTTLEDIAKLNKENKGLNLTSCDANTLPAWCAYSEKAR 270
249 STYDTKLSFPCCDFTHDEWINYDYLSKKYVGHGAGNPLGP*GGYGYANJEL-ARLTHSP 306
271 GYSDV-----CDITTEDELYRYSYGDQVSYFGDGPYGMIRSVGANLENAT-KLLKQSE 325
309 VHDOTSSNHTLDSPTAFPLNSLYADFSNDNIIISILFALG:YNGTKPLSTTTVENITC 368
326 TDD-----LKMVSFTHTCTD:LAVYATAGTIDCKNLTABYVFPNGN 367
365 TDGFSNAWTPPFASRLVYVEMNOCAGDEPVRV:VNDREVVELHGCPDVALGRCTRESF-- 426
369 T--FHKSYYVYQGARVTEKFOC--SNDTVRVYVINDAVVPEETCS*GPGFSCEINDFYD 423
427 -----VRGLSFAR 434
424 YAEKRVAGTDFLK 436

RESULT 5
PPAS YEAST
ID -PPAS YEAST STANDARD; PRT: 467 AA.
AC P00635;
DT 21-JUL-1986 (Ref. 31, Created)
DT 01-OCT-1994 (Ref. 30, Last sequence update)
DE Repressible acid phosphatase precursor (EC 3.1.3.2) (P60).
GN PHO5 OR YBR03C OR YBR0814.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCBI_taxid=4932;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
RA Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
RT "The nucleotide sequence of the yeast PHO5 gene: a putative precursor
of repressible acid phosphatase contains a signal peptide.";
RJ Nucleic Acids Res. 11:1657-1672(1983).
[2]
SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
RA VESLINE=85037940; PubMed=6093051;
RA Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinner A.;
RT "Structural analysis of the two tandemly repeated acid phosphatase
genes in yeast.";
RL Nucleic Acids Res. 12:7721-7735(1984).
[3]
SEQUENCE FROM N.A.
RA STRAIN=S288C;
RX MEDLINE=95208357; PubMed=790426;
RA Mannhaupt G., Stucka R., Ehle S., Vetter T., Feldmann H.;
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
RL Yeast 10:1363-1381(1994).
[4]
SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=87064474; PubMed=3537710;
RA Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott O.E.,
RA Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.;
RT "Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene
cluster within the acid phosphatase multigene family of Saccharomyces
cerevisiae.";
RL Mol. Cell. Biol. 6:1855-1865(1986).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monester + H2O = ar.
alcohol + phosphate.

```

```

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: REPRESSIBLE BY INORGANIC PHOSPHATE.
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: V01320; CAA24630.1; .
DR FMSJ: X01079; CAA25555.1; .
DR EMRI: X78993; CAA55598.1; .
DR EMSJ: X35962; CAA85046.1; .
DR EMBJ: X01080; CAA25556.1; .
DR PIR: S05795; PABYC.
DR HSSP: P34755; IQFX.
DR SGD: S000297; PHO5.
DR GC: G00009277; Cereali wall (sensu Fungi); IDA.
DR GC: G00030287; Cereplasmic space (sensu Fungi); NAS.
DR InterPro: IPR000560; HisAc_Pheptase.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS-ACID-PHOSPHAT-1; .
DR PROSITE: PS00778; HIS-ACID-PHOSPHAT-2; .
KW Hydroxylase; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 17
FT CHAIN 18 467
FT ACT_SITE 75 75
FT ACT_SITE 337 337
FT CARBOHYD 97 97
FT CARBOHYD 103 103
FT CARBOHYD 162 162
FT CARBOHYD 192 192
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 356 356
FT CARBOHYD 390 390
FT CARBOHYD 439 439
FT CARBOHYD 445 445
FT CARBOHYD 456 456
FT CARBOHYD 461 461
FT CONFLICT 36 36
FT CONFLICT 130 130
FT CONFLICT 294 294
FT CONFLICT 446 446
FT CONFLICT 462 462
FT CONFLICT 466 466
SQ SEQUENCE 467 AA; 52858 MW; DC3C9504BC2D3CC CRC64;
Query Match 16.5%; Score 385; DB 1; Length: 467;
Best Local Similarity 26.2%; Pred. No. 1.2e-21;
Matches 1.4; Conservative 66; Mismatches 189; Indels 66; Gaps 14;
QY 26 GOVAPFESLANESVSPVACRVTFQAQLSRHGARYFTDSKGYKYSALIEIQQNATF 85
DB 42 GGAGPYISFGDYG-SRDLPECEKQLQWVGHERYPTVSLAKTISKTWKLSNYTRQ 101
QY 86 FQGYAFLEK-TYNSYLGADD-----LTPF-GEQELVNSGKIFQRYESLTR 129
DB 102 FNGSLFLNDYEFFIRDDDDLEMETTFANSDVLPYTGEMAKHAREFLACYGYVVE 161
QY 130 NVVPF-IRSSGSRVSIAGKKFIEGPOSTKJOPRAQPGSSFKIDVSEASSNNTLD 188
DB 162 NQTSFAVFTSNKRCHDTAQYFDG-----LGD-----QFN-TLQTVSEAESAGANTLS 210
QY 189 P-GCTVFEDSELADTVEANTATATVPVSIORJENLDSGLTDTTEVTLMDYCSFDTIS 247
DB 211 ACNCSFAM-DYDANDDINVEYDTTYDDIAKLNKENKGLNLTSDASTFLFWCAFE--- 266
QY 248 TSTVDTK-LSPFCDLFTHDEWINYDYLSKKYVGHGAGNPLGPQGVGYANJEL-ARLTH 306

```

```

Db 267 ---VNAKGVSDVCDITFKDELVHYSVYQDLHYYHGGPOVD::KSGVGNLNFASVXLLKQ 323
QY 307 SPVDDTSSNHTLSSSPATFFPLNSTLYARDFSHNGHIIISILFAGLYNCTKPK:STTTVENI 366
Db 324 SE:QC-----QKWLSTFTHDTC:INFLLTAGT::DDKNLTAEYVPPFM 365
QY 367 TOTDGFSSAWTVFASRLVYVMMQCAOEPLVVLVNDVVVPLKGPVDALGRCCTROSF 426
Db 366 GNT--PHRSNYVQGARVYTERFQC--SNDTVRVVINDAVVFEETCSTGGFSCSE:NDP 421
QY 427 -----VRGLSPAR 434
Db 422 YDVAEKRVAGTDLK 436

```

RESULT 6

```

PPAD_YEAST STANDARD; PRT; 468 AA.
AC P52290;
DT 01-OCT-1996 (Rel. 34, Created:
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Probable acid phosphatase YD024C precursor (EC 3.1.3.2).
GN YD024C OR D2815.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Andre B., Vissers S., Urrestarazu L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

SQ SEQUENCE 468 AA; 53076 MW; 1F07FF374DDF-62C CRC64;
Query Match 15.8%; Score 368; DB :; Length 468;
Best Local Similarity 25.0%; Pred. No. 2.3e-20;
Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;
QY 26 GQVAPFESLANESVISPVPACRVTFQAQLSRGARYPTDSKGGKYSALIEE:QQNATT 85
Db 43 GGSAPFESPNYGYPTDIPGCR:TCVQM:GRHGRYFTRSEAKC:FEVWYK:SNYTGK 102
QY 86 FDKYAFALKT:YNYSJ-----GADLTPF-GECELVNSGKIKYQRYESUTR 129
Db 103 YEGSLSLNNGYEFTPDESLEEMETT:QNSIDVLNPLYTGEMNAKRHAREFLAKYGLME 162
QY 130 NIVFP-IRSSGSRVIAAGKKPE---GFGSTKLKPRAPQGGSSPKIDVIVSEASSN 184
Db 163 NCTNPFITNSKRIYDTAQYPAEALGGGNIS-----LQTSNSSSGA 207
QY 185 NTLDPOTCTVFEDSELAOTVEANFTATFVPS:ROSLENDLSGVTLTDT:EVTYLMDXGSPD 244
Db 208 NTLAAKSSCPMNSNANNDILMSYSDYLENISDRLENDKGLNLSRDAALFSCWAFE 267
QY 245 TISTSTVDTK-LSPECDL:FTHDEW:NYDYLQSLKKYGHGAGNPLGPTQGVGYANELIAR 303
Db 268 -----LNAGKYSNICDIPSAELIHYSYETDLSYFYQNGPGYKLIKSIGANLFRATV-K 320
QY 304 LTHSPVHDDTSSNHTLSSSPATFFPLNSTLYADFSHDNGIISILFAGLYNCTKPK:STTTV 363
Db 321 LIRQSAH-----LDQKWLSTFTHDTC:INFLLTAGT:DDKNLTAEYVPPFM 365
QY 364 EN:TOTDGFSSAWTVFASRLVYVMMQCAOEPLVVLVNDVVVPLKGPVDALGRCCTR 423
Db 364 P--FRDHSYHRSWY:POGARVYTERFQC--SNDTVRVVINDAVVFEETCSTGGFSCSE 419
QY 424 DSP-----VRGLSPF 432
Db 420 GFYEYAKDLRGVSP 435

```

RESULT 7

```

PPAD_YEAST STANDARD; PRT; 467 AA.
AC P35842;
DT 01-JUN-1994 (Rel. 29, Created:
DT 01-JUN-1994 (Rel. 29, Last sequence update);
DT 01-NOV-1997 (Rel. 35, Last annotation update);
DE Acid phosphatase PHO1 precursor (EC 3.1.3.2) (P561).
GN PHO1 OR YAR071W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RC MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong M., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Quellet E.F.P., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms A.K.;
RA "The nucleotide sequence of chromosome I from Saccharomyces
RA cerevisiae";
RA Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
[2]
SEQUENCE FROM N.A.
RA Chen J.Y., Gong Y.I., Ao S.Z.;
RA "The primary structure of acid phosphatase gene PHO1 in S.
RA cerevisiae and comparison with other gene families.";
RA Acta Biochim. Biophys. Sin. 21:437-444(1989).
CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate
CC -1- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS
CC CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
CC -1- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.

```

CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL: L28920; AAC09508.1; -

DR EMBL: U19789; AAA73479.1; -

DR PIR: S53476; S53476.

DR HSSP: P34755; ICPI.

DR SGD: S000094; PHO1.

DR GO: GO:0005576; C:extracellular; IDA.

DR GO: GO:0003993; F:acid phosphatase activity; IDA.

DR InterPro: IPR000560; HisAc_phsptase.

DR Pfam: PF00128; acid phosphatase.

DR PROSITE: PS00616; HIS-ACID-PHOSPHAT_1; -

DR PROSITE: PS00778; HIS-ACID-PHOSPHAT_2; -

KW Hydroxylase; Glycoprotein; Signal; Multigene family.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 467 ACID PHOSPHATASE PHO1.

FT ACT_SITE 75 75 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).

FT ACT_SITE 337 337 PROTON DONOR (BY SIMILARITY).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT A -> L (IN REF. 2).

FT VS -> AR (IN REF. 2).

FT R -> H (IN REF. 2).

FT K -> Q (IN REF. 2).

FT D -> G (IN REF. 2).

SQ SEQUENCE 467 AA; 52757 MW; AECDC1C946B326C3 CRC64;

Query March 15.18; Score 352; DB 1; Length 467;

Best Local Similarity 24.4; Pred. No. 3.7e-19;

Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 26 GQVAPFFSLANESVISPEVAGCRVTFQAQLSRHGARYPTDSKGGKYSALIEEIQQVAT 85

DB 42 GSGSPYSPFCGYISRLPESCEMKQVMGRIGERYPTVSKAKSINTWYKLSNWTGQ 101

QY 86 PDGYAFK-----TNYSL-----GADLTFF-GEQELVNSGKIFYORYESLJR 129

DB 102 PFGALSFENDYEFPIRDTKNLEMTLLANSVNLNPTTGEMNAKHARDFLAQYGYMVE 161

QY 130 NIVPF-IRSSGSSRVIASGKFFIEGFSQTKLKDPAQCGOSSPIDV---VISEASSN- 184

DB 162 NQTSFAVFTSNRCHDTAQFIQGL-----GKFNLSLQTISEASAGA 256

QY 185 NTLDP-GTCTVFESSEADTVEAKFTATFVPSIFQRLENDLSGVTLTIDTETVLMDCSF 243

DB 207 NTLNAAHSCPAKDD-DVNDL-LKYVDIKYLSG-AKLNKENKGLNLTSSDAN-FFAKCAY 265

QY 244 DTISTSTVDTKLSFCDLFTHDEWINDYDLSKKYKYGCHAGNPLGPTQGVGVANELIAR 303

DB 266 EINARG-----YSDICNIFTDELVRFSYGOLETYYQTGPGVWRSVGNK-FNASVKL 320

QY 304 LTHSPVHDDTSSNHTLSSSPA7FPLNSTLYADFSHDNGI-SILFALGLYNGTKELSTTY 363

DB 321 LKSEVQD-----QKWLSPF-HDTDLNLYLTIGIDDKXNKLTAHV 362

QY 364 ENIQTDGFSASWTVPFASRLYVEMMOCAQBEPLVRLVNDRVVPLHGGCFVDAIGCTR 423

DB 363 PPMENT--FHRSWYVPCQARVYVTEKQC--SNDFTVRYVINDAVVPIETCTSGPGSCFI 418

QY 424 DSF-----VRG-SFAR 434

DB 419 NDFDYDAEKRVAGTDFLX 436

RESULT 8

PPAC_YEAST STANDARD; PRI: 467 AA.

AC P38593;

DT 01-FEB-1995 (Rel. 31; Created;

DT 01-FEB-1995 (Rel. 31; Last sequence update)

DT 01-FEB-1995 (Rel. 31; Last annotation update)

DE Acid phosphatase PHO1.2 precursor (EC 3.1.3.2).

GN PHO12 OR YHR215W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RR [1]

RF SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;

RX MEDLINE=94378003; PubMed=8991229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favello A., Fulton J., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Lier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser J.,

RA Nhan M., Rifkin J., Riles L., St Peter H., Trevisan E., Vaughan K.,

RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

RA Vaudin M.

RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

RT VII."

RL Science 265:2077-2082(1994).

CC -- CATALYTIC ACTIVITY: An orthophosphoric monoester - H₂O = an

CC alcohol + phosphate.

CC -- INDUCTION: S-CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS

CC CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.

CC -- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE FAMILY.

CC -- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL: L00029; AAB69729.1; -

DR PIR: S4896; S4896.

DR HSSP: P34755; ICPI.

DR SGD: S0001258; PHO12.

DR InterPro: IPR000560; HisAc_phsptase.

DR Pfam: PF00328; acid phosphatase.

DR PROSITE: PS00616; HIS-ACID-PHOSPHAT_1; -

DR PROSITE: PS00778; HIS-ACID-PHOSPHAT_2; -

KW Hydroxylase; Glycoprotein; Signal; Multigene family.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 467 ACID PHOSPHATASE PHO1.

FT ACT_SITE 75 75 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).

FT ACT_SITE 337 337 PROTON DONOR (BY SIMILARITY).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 467 AA; 52699 MW; BEC6C6CDF39B845B CRC64;

Query Match 15.1%; Score 352; DB 1; Length 467;
 Best Local Similarity 24.4%; Pred. No. 3,7e-19;
 Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 26 GQYAPFFSLANESVISPEVAGCRVTFPAQLSRHGRARPTDSKKYKAL-EE-QQNAIT 85
 DB 42 GSGSPYVSPGDIYGRDLFESCEMKGQVWSPHGERVPTSKAKSIYTTKYLKSNYTGQ 101
 QY 86 FDCRYAFK-----TNYSL-----GADDLTPF-GEOLVNSGKIFYQVES:TR 129
 DB 102 FSGALSFNDYDFEIRDTKLEMETELANSYVNLNPTGEMAKRHARDFLAQGYNVE 162
 QY 130 NIVPP-IRSSGSRV-ASGKKFIEGQSTKCDPRAQPOSSPKIDV---VISEASSN- 184
 DB 162 NCTSPAVFTSNRCHDTAOFYDGL-----CDKENISLCIISAESAGA 206
 QY 185 NTLDP-GTCVFESELAOTVEANFTATVPISIRORLNDLSGVTLTDEVTYLMDCSF 243
 DB 207 NTLASHSFPAWD-DVNDLILKYYCTKYLSGIKAKLNKENKGLNLTSSDANTTFAMCAY 265
 QY 244 DT-STSTVCRKLSPPFCOLPHDEMINYDLOS-KKYYGHGAGNPLGPTCGVGYANELIAR 303
 DB 266 EINARG-----YSDICNIFKDELVPFSYQDLE-YVQTGPGYDVVRSGANLFNASVKL 320
 QY 304 LTHSPVHDOTSSNHTLSSPATPPLNSTLYADPFSHENGIIIS-LFALGLYNGEKLSTTTV 363
 DB 321 LKSEVQD-----QKWLSTHTD-LNYLTITIGIICDQNNLTAEHV 362
 QY 364 ENITQDGFSSAMTVPASRLVYEMOCCAEPELVLVNDRVVPLHCGCPVDALGRCTR 423
 DB 363 PFHENT--FHSRYVPGARVYTEKFC--SNITYVYVINDAVPIETCTGPGFSCF: 418
 QY 424 DSF-----VRGLSFAR 434
 DB 419 NDFGYAEKRVAGTDFE-K 436

RESULT 9
 PFA5_KULUA STANDARD; PRT; 469 AA.
 AC P32289;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Repressible acid phosphatase precursor (EC 3.1.3.2).
 GN P305.
 OS Kluyveromyces lactis (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 CC NCB: TaxID=28985;
 RN 1;
 RC STRAIN=CBS 2359/152;
 RA Ferminan E.;
 RJ Thesis (1995); University of Salamanca, Spain.
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H2O = an
 CC alcohol + phosphate.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
 CC -!- PM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; 233995; CAAB3964.1; --
 CC FSSP; P34755; 1QFX.

DR IcterPro; IPR000560; HisAc_Phasphatase.
 DR Pfam; PF00128; acid_phosphat; 1.
 DR PROSITE; PS00416; H-S-ACID-PHOSPHAT; 1.
 DR PROSITE; PS00778; H-S-ACID-PHOSPHAT; 1.
 KW Hydroxylase; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 16
 FT CHAIN 17 469
 FT REPRESSIBLE ACID PHOSPHATASE.
 FT ACT_SITE 77 77
 FT NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 339 339
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 23 23
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 31 31
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 32 32
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 129 129
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 201 201
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 229 229
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 250 250
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 317 317
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 332 332
 FT N-LINKED (GLCNAC).
 FT CARBOHYD 447 447
 FT N-LINKED (GLCNAC).
 SQ SEQUENCE 469 AA; 52532 MW; 863B528D0740AA7E CRC64;

Query Match 15.0%; Score 351; DB 1; Length 469;
 Best Local Similarity 24.8%; Pred. No. 4.5e-19;
 Matches 119; Conservative 66; Mismatches 177; Indels 118; Gaps 17;

QY 12 DQGYOCF-----SETSLMQYAPFFSLANESVISPEVAGCRVTFPAQV-SRHGR 62
 DB 22 DNGTCYALNNSTTDESIFSLNQ-GPHYDYPQSFGIPVEVPDQCTVEHVQMLARHGR 80
 QY 63 YPTDSGKKYKYSALIEIQONAT--EDGKAFUKTYNSLGADDLTPFGSOELVNSGIFQY 122
 DB 91 YPTASGKLMIALMDKLE---FQGY-----NDPLEVFNDFEYFVSNTKYFD 125
 QY 123 R-----YESLRNIVPFISSGSSRVSIAKKEFEG 153
 DB 126 QLTNSTVDPSNPYAGAKTAQHLGKYIAYNYGDLFSDSNPVF--SS-SGRVHCTAKYVVSS 184
 QY 154 FOSTKLDPRAQPGQSSPKIDV-----VISEASSN-NTLDPGTCTVFESESLADTVEAN 207
 DB 185 LEE-----ELDQLDQL:IQENETSGANSLTPADSCMTYNGSLGDEYFEN 229
 QY 208 F-TATVPVPSIRQ--LERULSGVTITDTEVTYLMDCSFDTITSTVTKLSPPFCOLYTHD 265
 DB 230 ATLPLYLTDKNEMKKNLNLTLEHDDIELVDWCAFE:VWKS-----SAYCDLFERN 284
 QY 266 EMINCYLOSLLKYYCHGAGNPLGPTCGVGYANELIARLTHSPVHDOTSSNHTLSSPAT 325
 DB 285 DLVAYSYYANVNFYRGGAGNPMSPGSGVJNAYNKLTCQD----- 327
 QY 326 FPLKSTLYADPFSHENGIIISLFALGLY-NGTKPLSTTTV--ENITQDGFSSAMTVPFAS 382
 DB 325 -ELDNKWLFSFSDTDICCFISALGLIDNGVTEYSLDQDFONICOL-----SWTPMG 381
 QY 383 RLYVENMOCQAEQELVRLVNDRVVPLHCGCPVDALGRCTRCSF-----VRGLSFAR 435
 DB 382 RIPTKLEK--GMASYVRYINDVPIPVGCTSGPGFSCFIEDFDQVCTNRLNGIDYVSS 439

RESULT 10
 PFB5_ASFNG STANDARD; PRT; 479 AA.
 AC P34754;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
 DE 3-phosphohydrolase B) (3 phytase B) (Myo-inositol hexakisphosphate
 DE 3-phosphohydrolase B).
 GN PFB5.
 OS Aspergillus niger.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 CC NCB: TaxID=5061;

```

RN [1]
R2 SEQUENCE FROM N.A., AND SEQUENCE OF 20-201; 133-241 AND 376-399.
RX MDLNAME=93371452; PubMed=7916610;
RA Erlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
RA Ullah A.H.J.;
RT "Identification and cloning of a second pyruvate gene (pyrB) from
RL Aspergillus niger (ficusum)";
RL Biochem. Biophys. Res. Commun. 195:53-57(1993).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H2O = 1D-
CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; J20567; AAA02334.1; .
CC HSP; P34755; 10FX.
CC InterPro; IPR000560; HisAc phosphatase.
CC Pfam; PF003328; acid phosphatase.
CC PROSITE; PS00616; HIS-ACID-PROSPHAT_1; 1.
CC PROSITE; PS00778; HIS-ACID-PROSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 479 3-PHYTASE B.
CC ACT_SITE 81 81
CC
CC ACT_SITE 82 82
CC ACT_SITE 337 337
CC CARBOHYD 106 106
CC CARBOHYD 191 191
CC CARBOHYD 227 227
CC CARBOHYD 250 250
CC CARBOHYD 315 315
CC CARBOHYD 425 425
CC CARBOHYD 442 442
CC CARBOHYD 458 458
CC SEQUENCE 479 AA; 536.1 MW; 39504DA2950DFC4 CRC64;
Query Match 14.5%; Score 339.5; DB 1; Length 479;
Best Local Similarity 27.9%; Pred. No. 3.4e-18;
Matches 109; Conservative 60; Mismatches 165; Indels 57; Gaps 15;
QY 40 ISPEVAGCRVTAQVLNRHRCARYPTDSKQKY-SALIEEQQNATTFDQKYAPLTKYK 98
DB 63 IARDPTGCEVDQVIMYKRGERYPSPSAGKSTEEALAKYYSINT-EYKGLAFNDWTY 122
QY 99 SL-----GADDLT-PT-GQELVNSGIKFYQRYESL--TRNIVPFRSSGSRV-ASGK 148
DB 123 YVNECYNAETSGPAGLLDVAHNCNDYKARYGHLWGEVTVVPFF-SSGYGRVETAR 191
QY 149 KFTGFGOSTKLKPRAGPGSSPKIDVISEASSNNLTDPGCTCFVDESELAQTVANF 208
DB 182 KFGEGFGYKYN-----STNAALNIISESEVMGADSLTP-ICD'DNDQCT'CDNLTYQL 232
QY 209 TATFVPSIRORLENDVSGVTLTDTETVYVMDGSEFDISTSTVDTKLSPCDLFTHDEW 268
DB 233 PQFVAAARLNSQN--PQMNLTASDVNVLVMAFSFELNA-----RPFSNMINAFTQDEW 285
QY 269 NYCYLQSLKKYHGAGNPLGPTQGVGVANELARLTHSPVHEDTSNHTLDSPATFPL 328
DB 286 SFGVVDLNYCYACGPGDKQMAAGVAYANASLTINQGP-----KEAGP----- 330
QY 329 NSTLYADFSHNGTISILFALGLY--NGTKPLSTTTTVENITQDGFSSAWTVFASRLYV 386
DB 331 --LFFNFADHDTNITPILAAAGLVLPNEULPDRVAFGN-----FYSIGNIVPMGGLTI 382

```

```

QY 387 EYMQCOA----EQEPLVRVLVNDVRVPLHGC 413
DB 383 ERLSCQATLSDKGTYYRLVNLNEAVLPFND 413
RESULT 11
PHYB ASPAK
ID PHYB ASPAK STANDARD; PRT: 479 AA.
AC P34755;
DE 01-FEB-1994 (Rel. 28, Created)
DE 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE 3-PHYTASE B precursor (SC 3.1.3.8) (Myo-inositol-hexaphosphate
DE 3-phosphohydrolase B) (pH 2.5 optimum acid phosphatase).
DE PHYB OR AFB.
GN Aspergillus awamori.
OS Eukaryota; Fungi; Ascomycota; Peizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RE SEQUENCE FROM N.A.
RC STRAIN=ALKO243;
RX MEDLINE=94040796; PubMed=8224894;
RA Piddington C.S., Houston C.S., Palohelm M.T., Cantrell M.A.,
RA Viethinen-Oinonen A., Nevalainen H., Ramosek J.A.;
RT "The cloning and sequencing of the genes encoding phytase (phy) and
RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT awamori";
RT Gene 133:45-62(1993).
RE [2]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RP MEDLINE=99264417; PubMed=10329192;
RA Kasture D., Wyss M., E-Arcy A., van Loon A.P.;
RT "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
RT 2.4-A resolution";
RJ J. Mol. Biol. 288:945-974(1999).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H2O = 1D-
CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; J02420; AAA16897.1; .
CC FIR; JN0890;
CC PDB; 1QFX; 19-APR-00.
CC InterPro; IPR000560; HisAc phosphatase.
CC Pfam; PF003328; acid phosphatase.
CC PROSITE; PS00616; HIS-ACID-PROSPHAT_1; 1.
CC PROSITE; PS00778; HIS-ACID-PROSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Signal; 3D-structure.
CC SIGNAL 1 19
CC CHAIN 20 479 3-PHYTASE B.
CC ACT_SITE 82 82
CC ACT_SITE 337 337
CC DISULFID 71 387
CC DISULFID 128 472
CC DISULFID 216 441
CC DISULFID 225 298
CC DISULFID 413 421
CC CARBOHYD 191 191
CC CARBOHYD 315 315
CC CARBOHYD 458 458
CC HELIX 41 43
CC HELIX 45 47
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)

```


RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton C., Simmonds M., Squares R., Stevens S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA Weljers J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabler C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Potz T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purneille B.,
RA Coffeart A., Cadieu E., Dreano S., Gloux S., Delaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hurt C., Moore K., Hurst S.M.,
RA Lucab M., Pochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti J., Lowe T., McCombie W.R., Paulsen I., Paulsen J.,
RA Shpakowski G.V., Ussery D., Barrall B.G., Nurse P.,
RA The genome sequence of Schizosaccharomyces pombe.";
RA Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H2O = an
CC alcohol + phosphate.
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -!- INDUCTION: REPRRESSED BY PHOSPHATE AND WEAKLY BY THIAMINE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M11857; AAA35321.1; ..
CC EMBL: AL137099; CAB8657.1; ..
CC PIR: A25326; A25326.
CC HSP: P34355; IQFX.
CC GeneDB: Spombe; SPBP43.02; ..
CC InterPro: IPR00560; HisAc_phsphtse.
CC Pfam: PF0328; acid_phosphat; 1.
CC PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase: Glycoprotein; Cell wall; Signal.
CC SIGNAL 1 18
CC FT CHAIN 19 453 ACID PHOSPHATASE.
CC FT ACT_SITE 69 69 NCLEOPHILIC ACCEPTOR (BY SIMILARITY).
CC FT ACT_SITE 330 330 PROTON DONOR (BY SIMILARITY).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 151 151 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 193 193 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 243 243 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 319 319 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 410 410 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 429 429 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 443 443 N-LINKED (GLCNAC..) (POTENTIAL).
CC SEQUENCE 453 AA; 50557 MW; 7CF891256EB154D1 CRC64;
Query Match 12.7%; Score 296.5; DB 1; Length 453;
Best Local Similarity 24.5%; Pred. No. 5.6e-15;
Matches 103; Conservative 57; Mismatches 190; Indels 71; Gaps 12;
QY 18 FSETSHLWGO--YAPFESLANESVISPEV--PAGCRVTFACVLSHRGARYPTDSKGGKY 72
DB 30 FDFKELTSRSPYHKPYF-----YGPSDFPTTCIKQVTHLQHGSRNPTGSGNAFD 62
QY 73 SALIEEIQQ-----NATTFDGKAFUKTYN---YSLGADDTLPFGQELVNSGIRF 120
DB 83 AVGIANFQORLLNGSVPIDYVSGNPLSFVPTMTPTVIEAANAADALSSSGRVELFDMGRQF 142
QY 121 YQRYESLTRNIVPPIRSCGSRVIVASGKPF-----IEGFSTKLKDFRAQFGSSPK 172
DB 143 YERYHELNFNASTYNIYTAQQRVVDVSAALWYGVGMGVDVHNFNYILVSNATAGNS-- 200

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton C., Simmonds M., Squares R., Stevens S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA Weljers J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabler C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pott T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purcell B.,
RA Coffeart A., Cadieu E., Dreano S., Gloux S., Delaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hurt C., Moore K., Hurst S.M.,
RA Lucab M., Pochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti J., Lowe T., McCombie W.R., Paulsen I., Paulsen J.,
RA Shpakowski G.V., Ussery D., Barré B.G., Nurse P.,
RA The genome sequence of Schizosaccharomyces pombe.";
RA Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H2O = an
CC alcohol + phosphate.
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -!- INDUCTION: REpressed BY PHOSPHATE AND WEAKLY BY THIAMINE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M11857; AAA35321.1; ..
CC EMBL: AL137099; CAB8657.1; ..
CC PIR: A25326; A25326.
CC HSP: P34555; IQFX.
CC GeneDB: Spombe; SPBP43.02; ..
CC InterPro: IPR00560; HisAc_phsphtse.
CC Pfam: PF0328; acid_phosphat; 1.
CC PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase: Glycoprotein; Cell wall; Signal.
CC SIGNAL 1 18
CC CHAIN 19 453 ACID PHOSPHATASE.
CC FT ACT_SITE 69 69 NCLEOPHILIC ACCEPTOR (BY SIMILARITY).
CC FT ACT_SITE 330 330 PROTON DONOR (BY SIMILARITY).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 151 151 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 193 193 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 243 243 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 319 319 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 410 410 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 429 429 N-LINKED (GLCNAC..) (POTENTIAL).
CC FT CARBOHYD 443 443 N-LINKED (GLCNAC..) (POTENTIAL).
CC SEQUENCE 453 AA; 50557 MW; 7CF891256EB154D1 CRC64;
Query Match 12.7%; Score 296.5; DB 1; Length 453;
Best Local Similarity 24.5%; Pred. No. 5.6e-15;
Matches 103; Conservative 57; Mismatches 190; Indels 71; Gaps 12;
QY 18 FSETSHLWGO--YAPFESLANESVISPEV--PAGCRVTFACVLSHRGARYPTDSKGGKY 72
DB 30 FDFKELTSRSPYHKPYF-----YQPSDFPTCKIKQVTHLQHGSRNPTGSGNAFD 62
QY 73 SALIEEIQQ-----NATTFDGKAFUKTYN---YSLGADDTLPFGQELVNSGKIF 120
DB 83 AVGIANFQORLLNGSVPIDYVSGNPLSFVPTMTPTVIEAANAADALSSGRLVDFMDGRQF 142
QY 121 YQRYESLTRNIVPFISSGSRVIVASGKPF-----IEGFSTKLKDFRAQFGSSPK 172
DB 143 YERYHELNFNASTYNIYTAQQRVVDSSALWYGVGMGVDVHNFNYILVSNATAGNS-- 200

QY 173 IDWVISEASSNNLDPGTCVFESELDATVEANFTATFVFSRQRLNDLSGVTLOT 232
 DB 201 -----SSYN-----ACASDADDTTTPALAEWRNVWPPRQRLNPFYSYNKLTND 247
 QY 233 EYTVLMDMSFDTSTVTKLSPFCDLTHDEKINVDYLOSKKYVGHGAGNELQPTC 292
 DB 248 DILNLYGICSYEIALQC-----YSEFCKLNSVDNFNFEYSGDLFSYGMNSYKWSIF 322
 QY 293 GVGYNELARLTHSPVHDTSNHTLSSPATFPLNSTLYADESHDNGIISILFALGLY 352
 DB 303 GAYANSLANSR-----SVENNT-----QQFFAFTHDANKIPVETALGFF 344
 QY 353 NGTKPLSTTVENITQDGFSSAVTVPFASRYVEMMCQAEQFPVRLVNLRAVPELHG 412
 DB 345 TDNTPENPLPSTVGVHSHMSKASRPVPAGNLTLELPQCE-DSKYVVRHLVNEEVFLSD 403
 QY 413 C 413
 DB 404 C 404

RESULT 14
 PP22_SCHPO STANDARD: PRT: 463 AA.
 ID PP22_SCHPO
 AC Q01682; Q9U070;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Thiamine-repressible acid phosphatase precursor (BC 3.1.3.2).
 GN PH04 CR SP8C428.33C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
 RX MEDLINE=91064763; PubMed=2249257;
 RA Yang J., Schweingruber M.E.;
 RT "The structural gene coding for thiamine-repressible acid phosphatase
 RT in Schizosaccharomycetes pombe.";
 RL Curr. Genet. 18:269-272(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184840; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Spouris J., Peat N., Hayles J., Baker S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor A., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holois S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones S., Jones M., Leather S., McDonald S., McLean C.,
 RA Mooney P., Moule S., Mungall K., Murphy S., Niblett D., Odeli C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton C., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward C., Volckaert G., Aert R., Robben J., Grymprez B.,
 RA Weijtens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabe, C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann M., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreazo S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardier C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta C.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Petashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 RN [3]

SEQUENCE OF 1-71 FROM N.A.
 RC STRAIN=968 h30;
 RX MEDLINE=20222868; PubMed=10759889;
 RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
 RA Hiraoka Y.;
 RT "Large-scale screening of intracellular protein localization in living
 RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
 RL Genes Cells 5:169-193(2000).
 CC - FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
 CC - CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
 CC alcohol + phosphate.
 CC - SUBCELLULAR LOCATION: Cell wall.
 CC - INDUCTION: Repressed by thiamine.
 CC - SIMILARITY: BELONGS TO THE H-STEADY ACID PHOSPHATASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch)
 CC
 CC EMBL: X56939; CAA40258.1; --
 CC EMBL: AL034382; CAA22278.1; --
 CC EMBL: AB027777; BAA8708.1; --
 CC PIR: S14119; S14119.
 CC HSRP: P34755; 1QFX.
 CC GeneDB SPORBE; SPAC428.C3C; --
 CC InterPro: IPR000560; HisAc_phosphatase.
 CC Pfam: PF03328; acid_phosphat_1; 1.
 CC PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Cell wall; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 463
 FT ACT_SITE 69 69
 FT ACT_SITE 340 340
 FT CARBOHYD 98 98
 FT CARBOHYD 104 104
 FT CARBOHYD 186 186
 FT CARBOHYD 221 221
 FT CARBOHYD 251 251
 FT CARBOHYD 328 328
 FT CARBOHYD 433 433
 FT CARBOHYD 439 439
 FT CARBOHYD 458 458
 SO SEQUENCE 463 AA; 52118 MW; 748EAF8B55234A CRC64;
 Query Match 12.2%; Score 284; DB 1; Length 463;
 Best Local Similarity 24.9%; Pred. No. 5,1e-14;
 Matches 102; Conservative 56; Mismatches 181; Indels 60; Gaps 13;
 QY 28 YAPFSLANESVISPEVAGGRVTFQVLSHGARYP-----TDSKGYKYSALIE----- 77
 DB 43 HSPYNGEFTS-----PESCALQVH--LQRHGRNPTGDDTATDVSSAQVDFQNKLL 97
 QY 78 --EIQONATTFPGKVAFLKTNYSJ---GADLPFGCELVNSGKIFYORYESLTNIV 132
 DB 98 KGSIPVNFSEPNPYFVHWHTPVKAENAOQLSSGRZELFDLGRQVFEYEFJDTDV 157
 QY 133 PFISSGSRVIAAGKKEIEGFQSTKLMDPRAOFGCSKPIDVVI---SEASSNNLTDP 189
 DB 158 YDINTAAQERVVDSAEKWSYGVFGDDMN-----KCNFVLFEEDSAGANSAMY 207
 QY 190 GTCVFESESEL-ADTVEANFTA---TFVPSRQRLNDL-SCVTLTDTVETVYMDMSFD 244
 DB 208 YSCPVFENNIDENTTEAAHTSWANFLKPIANLNKYFDSGYNLTVSDVRSYVYICVE 267
 QY 245 TISTSTVETKLSPPCOLFTTHDEWINVDYLSLKKYVGHGAGNPLGPTGQGVYANETIARL 304
 DB 268 IALRNSD-----FCSLTFPSEFLNFEYDSDLDVAYWGPASEWASTLGGYVNNLANL 322

```
QY 305 THSPVHDTSSNHTLSSPATFENSTLYADFSHDNGIISILFALGSLVNGTTPFLSTTIVE 364
Cb 323 R-----KQVNASORK-----VFLAF-HDSQIIPVEAALGFPPDITPEHP-LPTD 366
QY 365 NITCTDGFSSAKTVFASRLYVEMMCOQAOEPLVAVLNDVRVPLHGC 413
Cb 367 KNIFTYSLKTSVPFAGNLTLEFLC-SNKYYVRLVNOQYPLTDC 414

RESULT 15
AGP_ECOLI
ID AGP_ECOLI STANDARD; PRT; 413 AA.
AC P1936;
D 01-FEB-1991 (Rel. 17, Created!
D 01-FEB-1991 (Rel. 17, Last sequence update)
D 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucose-1-phosphatase precursor (EC 3.1.3.10) (G:Parse).
GN AGP OR B1032.
OS Escherichia coli.
CC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
OX MCS1_taxid=562;
RN [1];
SEQUENCE FROM N.A., AND SEQUENCE OF 23-31.
RC STRAIN=K12;
MEDLINE=9013018; Pubmed=2151660;
RA Pradel E., Varck C., Boquet P.L.;
R "Nucleotide sequence and transcriptional analysis of the Escherichia
R coli agp gene encoding periplasmic acid glucose-1-phosphatase."
R J. Bacteriol. 172:802-807(1990).
RN [2];
SEQUENCE FROM N.A.
RC STRAIN=K-2 / MG1655;
RA MEDLINE=9742661; Pubmed=9278503;
RA Battner F.R., Plunkett G. J., Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
R "The complete genome sequence of Escherichia coli K-12."
R Science 277:1234-1238(1999).
RN [3];
SEQUENCE FROM N.A.
RC STRAIN=K12;
RA MEDLINE=97061202; Pubmed=8905232;
RA Chima T., Alba H., Baba T., Fujita K., Hayashi K., Horio A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara K., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Mizobuchi K.,
RA Nori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sasaki G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horikuchi T.;
R "A 7.8-kb DNA sequence of the Escherichia coli K-12 genome
R corresponding to the 12.7-28.0 min region on the linkage map."
R DNA Res. 3:137-155(1996).
RN [4];
SEQUENCE OF 23-34.
RC STRAIN=K12 / EMG2;
RA MEDLINE=97443975; Pubmed=9298646;
RA Link A.J., Robison K., Church G.M.;
R "Comparing the predicted and observed properties of proteins encoded
R in the genome of Escherichia coli K-12."
R Electrophoresis 18:1259-1313(1997).
CC -!- FUNCTION: ABSOLUTELY REQUIRED FOR THE GROWTH OF E. COLI IN A HIGH-
CC PHOSPHATE MEDIUM CONTAINING G-1-P AS THE SOLE CARBON SOURCE.
CC -!- CATALYTIC ACTIVITY: D-glucose 1-phosphate + H2O = D-glucose +
CC phosphate.
CC -!- ENZYME REGULATION: INDEPENDENT FROM INORGANIC PHOSPHATE
CC AVAILABILITY, AND APPARENTLY SUBMITTED TO CATABOLITE REPRESSION.
CC IT IS POSITIVELY CONTROLLED BY CAMP AND THE CAMP RECEPTOR PROTEIN.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- MISCELLANEOUS: OPTIMALLY ACTIVE AROUND PH 4.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
```

```
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M33807; AAA23426.1;
DR EMBL; AEC00202; AAC74087.1;
DR EMBL; D90737; BAA35769.1;
DR EMBL; D90738; BAA35779.1;
DR DDB; JY0087; JY0087.
DR HSP; F07102; LDKV.
DR EcoGene; EG-0033; agp.
DR InterPro; IPR003560; H:Sac phosphatase.
DR Pfam; PF00328; acid phosphatase.
DR PROSITE; PS02616; HIS-ACID-POSPHAT-1; 1.
DR PROSITE; PS02778; HIS-ACID-POSPHAT-2; 1.
KW Hydrolyase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1..22
FT CHAIN 23..413
FT ACT_SITE 40..40
FT ACT_SITE 311..311
FT ACT_SITE 311..311
SQ SEQUENCE 413 AA; 45683 MW; ADADAD3639D0D6AB CRC64;

Query Match 5.18; Score 119.5; DR 1; Length 413;
Best Local Similarity 22.04; Freq. No. 0.2; Indels 155; Gaps 22;
Matches 101; Conservative 40; Mismatches 163;

QY 44 VFAGRVTFACVLSRHGARVPTSGKSKYKSALEIEICQNTATTCGKYAFKTYNYSIGAD 103
DB 25 VFEQVQLCQVLMKSRHNPAPLANNG---SVLEQSTPN-----KWFEWYVGG 69
QY 104 DLTFFG-----EQELVNSG-----IKFYCRYSLTNNVFFIRSSGSR 142
DB 70 QLTTKGVLEVNGHYMREMLAEQGVKSGSCPPYTVYAYANSL-----QR 116
QY 143 VIASGKKEEGFQSTKLKDPAPQSGSSPKIDVWSEASSNNITLDRGCTVFEDELAD 202
DB 117 TVATAQFFITG-----AFPGCDP-----VHHQKMGTMPTFNVITDD 156
QY 203 TVEANFTATFVPSIRQRIENDLSGVTLTDT-----VTYL-----MDMCSF-----DT 245
DB 157 -----SNAFSEQAVAAVEKELSKLQITDSVQLLEKIVNPKDSACKKOCSSVDGKNT 210
QY 246 IS-----TSTVDTKLSPFDLFTHDE--W-----INYLQSLKKYVG 281
DB 211 FSARYQCEPPGVSGPELKVNSVDFAFTQYVEGFPYDQVAKGEKSDQDQWYVSKLXGYQ 270
QY 282 HGAGNPLGPTQGVYANELIARLTHSPVHDTSSNHTLSSPATFPLNSTLYADFSHDNG 341
DB 271 DSLFT--SPEVARNVAKPLVSVIDKALVTRTSA-----PKITVL-----VGHDSN 314
QY 342 IISILFALGLYNGTKPLSTTTTVENITQDQ--FSSANTVPFASR--LYVEKMQQAS--- 394
DB 355 IASLITALDF----KPYQLHDPQNETPIGKIVFORWHDGSKANRLMKIEVYVQSAEQLR 370
QY 395 -----QEPLVRVLVNDVRVPLHGCPCVDAIGRCTRDSF 426
DB 371 NADALTLOAPAQRV-----TLELSGCPDADGFCFMDKF 404

Search completed: November 12, 2003, 14:31:56
Job time : 19 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 12, 2003, 14:29:50 ; Search time 21 Seconds
(without alignments)
2033.281 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRNOSSCDTVQGYCCPSE.....SFVFGJSPARSGGWAECFA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 203000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	467	1 JN0656	3-phytase (EC 3.1.1.1)
2	2315	99.2	441	1 JN0482	3-phytase (EC 3.1.1.1)
3	2290	99.1	467	1 JN0889	3-phytase (EC 3.1.1.1)
4	385	16.5	467	1 PABYC	acid phosphatase (EC 3.1.3.8)
5	385	16.5	467	1 PABYC	acid phosphatase (EC 3.1.3.8)
6	368	15.8	468	2 S52495	acid phosphatase (EC 3.1.3.8)
7	352	15.1	467	2 S53476	acid phosphatase (EC 3.1.3.8)
8	352	15.1	467	2 S48996	acid phosphatase (EC 3.1.3.8)
9	337.5	14.5	479	1 JN0715	3-phytase (EC 3.1.1.1)
10	336.5	14.4	479	1 JN0890	acid phosphatase (EC 3.1.3.8)
11	327	14.0	468	2 C4285	acid phosphatase (EC 3.1.3.8)
12	300	12.9	463	2 J39929	thiamin-repressib.
13	296.5	12.7	453	1 A25326	acid phosphatase (EC 3.1.3.8)
14	284	12.2	463	2 S14119	acid phosphatase (EC 3.1.3.8)
15	148	6.3	468	2 A86233	hypothetical prote
16	132.5	5.7	465	2 JF3369	histidine acid pho
17	120.5	5.2	413	2 F93773	periplasmic glucos
18	120.5	5.2	413	2 B95636	periplasmic glucos
19	119.5	5.1	413	2 JY0087	glucose-1-phosphat
20	119	5.1	449	2 T15933	hypothetical prote
21	115	4.9	590	2 H75230	oligosaccharidase
22	114.5	4.9	1756	2 S45867	3-phytase (EC 3.1.1.1)
23	114	4.9	438	2 S64682	acid phosphatase (EC 3.1.3.8)
24	111.5	4.6	694	2 J40866	exo-alpha-stalidas
25	111.5	4.8	1032	2 F34433	hypothetical prote
26	111	4.6	1816	2 F83902	hypothetical prote
27	107	4.6	344	2 B89130	protein F52E1.8 (i
28	107	4.6	553	2 T06179	myb-related protei
29	107	4.6	1322	2 H86196	hypothetical prote

ALIGNMENTS

RESULT :

CN0656

3-phytase (EC 3.1.1.3.8) A precursor - Aspergillus niger

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase, phyaA protein

C:Species: Aspergillus niger

C>Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999

C:Accession: JN0656; S28456

R:van Hartingsveldt, W.; van Zeijl, C.M.C.; Hartveid, G.M.; Gonka, R.J.; Suykerbyk, A.M.J.

Gene 127, 87-94, 1993

A:Title: Cloning, characterization and overexpression of the phytase-encoding gene 'p

A:Reference number: JN0656; XCID:93252284; PMID:8197447

A:Accession: CN0656

A:Molecule type: DNA

A:Residues: 1-467 <VAN>

A:Cross-references: GB:21614; MID:92392; PID:CAA78904.1; PID:92393

A:Experimental source: strain NRRL335

A:Note: parts of the sequence, including the amino end of the mature protein, were co

C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and

C:Genetics:

A:Gene: phya

A:Introns: 15/2

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; p

F:1-23/Domains: signal sequence #status predicted <SIG>

F:24-467/Product: 3-phytase A #status experimental <MAT>

F:27,59,105,120,207,230,339,352,376,386/Binding site: carbohydrate (Asn) (covalent): #

F:61,361/Active site: Arg, His #status predicted

F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 100.0%; Score 2334; DB 1; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.7e-133;

Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASRNOSSCDTVQGYCCPSESHLWGQVAPFFSLANESVISPEVPAGCRVTFACVLSRHG 60

Db 24 ASRNOSSCDTVQGYCCPSESHLWGQVAPFFSLANESVISPEVPAGCRVTFACVLSRHG 83

Qy 61 ARYPTDSKGGKYSALIEIQNATTFDGKYAFLKTYNYSGLGADLTPEGEELVNSGIKF 120

Db 84 ARYPTDSKGGKYSALIEIQNATTFDGKYAFLKTYNYSGLGADLTPEGEELVNSGIKF 143

Qy 121 YORYESLNRNVPPFIRSSGSSRVIASGKKFEGQSTKLKDPRAQPGQSSPKIDVWISSEA 180

Db 144 YORYESLNRNVPPFIRSSGSSRVIASGKKFEGQSTKLKDPRAQPGQSSPKIDVWISSEA 203

Qy 181 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 240

Db 234 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 263

Qy 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

Db 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

Qy 181 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 240

Db 234 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 263

Qy 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

Db 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

Qy 181 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 240

Db 234 SSSNNTLPGTCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLLTDEVTYLMDM 263

Qy 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

Db 241 CSFDTISSTVDTKLSPECDFTHDEWNYDYJASLKYYGHGAGNPLGPTGGVYANEL 300

```

Db 264 CSPTTISTSTVETKLSPEFCDLTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 323
Qy 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
Qy 361 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 420
Db 384 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 443
Qy 421 CTRDSFVRGLSFARSGGDWAE 444
Db 444 CTRDSFVRGLSFARSGGDWAE 467

RESULT 2
JN0482
3-phytase (EC 3.1.3.8) A - Aspergillus ficuum
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phytA protein
C:Species: Aspergillus ficuum
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: JN0482; PM0023
R:Ullah, A.H.; Dischinger Jr., H.C.
B:Chem. Biophys. Res. Commun. 192, 747-753, 1993
A:Title: Aspergillus ficuum phytase: Complete primary structure elucidation by chemical
A:Reference number: JN0482; MUID:93249451; PMID:8387289
A:Accession: JN0482
A:Molecule type: protein
A:Residues: 1-441 <JUL>
A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
R:Ullah, A.H.; Cummins, B.J.; Dischinger Jr., H.C.
B:Chem. Biophys. Res. Commun. 178, 45-53, 1991
A:Title: Cyclohexanone modification of arginine at the active site of Aspergillus fic
A:Reference number: PM0023; MUID:9298982; PMID:1648914
A:Accession: PM0023
A:Molecule type: protein
A:Residues: 48-70 <U2>
C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F:436,82,97,194,207,316,329,335,365/Binding site: carboxylate (Asn) (covalent) #status
F:59/Active site: Arg, His #status predicted
F:59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 99.2%; Score 2315; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.3e-162;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASRNQSSCDTVDOGYQCFSETSHLWQYAPFFSLANESVLSPEVPAGCRVTFACVLSRHG 60
Db 1 ASRNQSSCDTVDOGYQCFSETSHLWQYAPFFSLANESVLSPEVPAGCRVTFACVLSRHG 60
Qy 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 120
Db 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 120
Qy 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 120
Db 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 120
Qy 121 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 180
Db 121 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 180
Qy 121 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 180
Db 121 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 180
Qy 181 SSSNNTLDPGCTVFEDSELADTVANFTATFVPSIRQRLENDSGLVTLTDEVTYLMQM 240
Db 181 SSSNNTLDPGCTVFEDSELADTVANFTATFVPSIRQRLENDSGLVTLTDEVTYLMQM 240
Qy 241 CSFDTISTSTVDTKLSPPCDLTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
Db 241 CSFDTISTSTVDTKLSPPCDLTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
Qy 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Qy 361 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 420

```

```

Db 362 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 420
Qy 421 CTRDSFVRGLSFARSGGDWAE 441
Db 421 CTRDSFVRGLSFARSGGDWAE 441

RESULT 3
JN0859
3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phytA protein
C:Species: Aspergillus awamori
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0859
R:Poddington, C.S.; Houston, C.S.; Palohelmo, M.; Castrell, M.; Miettinen-Oinonen, A.
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op
A:Reference number: JN0859; MUID:94040796; PMID:8224894
A:Accession: JN0859
A:Molecule type: DNA
A:Residues: 1-467 <PID>
A:Cross-references: GB:L02421; NID:G:66519; PID:AAA16998.1; PID:G:66519
A:Experimental source: strain ALK0243
A:Note: part of the sequence, including the amino end of the mature protein, was conf
C:Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic
C:Genetics:
A:Gene: phytA
A:Introns: 15/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-467/Product: 3-phytase A #status experimental <MAT>
F:27,59,105,120,207,230,339,352,376,382/Binding site: carboxylate (Asn) (covalent) #
F:81,361/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 98.1%; Score 2290; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 6.1e-160;
Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASRNQSSCDTVDOGYQCFSETSHLWQYAPFFSLANESVLSPEVPAGCRVTFACVLSRHG 60
Db 24 ASRNQSSCDTVDOGYQCFSETSHLWQYAPFFSLANESVLSPEVPAGCRVTFACVLSRHG 82
Qy 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADCLTFPGQEELVNSGIXF 143
Qy 121 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 180
Db 144 YQRYESLRTNIVPFISSGSRVTSAGKKFTEGQSTKXDPRAQPGQSSPKIDVWVISEA 202
Qy 181 SSSNNTLDPGCTVFEDSELADTVANFTATFVPSIRQRLENDSGLVTLTDEVTYLMQM 240
Db 204 SSSNNTLDPGCTVFEDSELADTVANFTATFVPSIRQRLENDSGLVTLTDEVTYLMQM 263
Qy 241 CSFDTISTSTVDTKLSPPCDLTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 300
Db 264 CSFDTISTSTVDTKLSPPCDLTHDEWINDYLOSILKKYVGHGAGNPLGPTQGVYANEL 323
Qy 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
Qy 361 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 420
Db 384 TTVENITQTQGFSSAWTVFPASRLYVEMMQCAEQEPLVRVLVNDRWVPLHGCPCVDALGR 443
Qy 421 CTRDSFVRGLSFARSGGDWAE 444
Db 444 CTRDSFVRGLSFARSGGDWAE 467

```

RESULT 4

ABYCC
acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093C
C:Species: *Saccharomyces cerevisiae*
C>Date: 19-Feb-1984 #sequence revision 30-Sep-1991 #text change 12-Nov-1999
A:Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27
R:Ba'wa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A:Reference number: S05794; MUID:85037940; PMID:6093051
A:Accession: S05795
A:Molecule type: DNA
A:Residues: 1-467 <BAW>
A:Cross-references: EMBL:X01079; NID:94162; PIDD:CAA25555.1; PIDD:9759282
A:Note: the authors translated the codon TAC for residue 272 as Ttr
A:Accession: A38792
A:Molecule type: Protein
A:Residues: 18-45 <BAW2>
R:Mannhaupt, G.; Stucka, R.; Ehle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A:Reference number: S48255; MUID:95208357; PMID:7920426
A:Accession: S48260
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-467 <MAN>
A:Cross-references: EMBL:X78993; NID:9476045; PIDD:CAA65598.1; PIDD:9536365; GSPDE:GN5000
R:Arima, K.; Osima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
Nucleic Acids Res. 11, 1657-1672, 1983
A:Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repress
A:Reference number: A00777; MUID:83168913; PMID:6300772
A:Accession: A00777
A:Molecule type: DNA
A:Residues: 1-35, 'V', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467 <AR
A:Cross-references: EMBL:V01320; NID:94158; PIDD:CAA24630.1; PIDD:94159
A:Accession: A38793
A:Molecule type: protein
A:Residues: 18-26, 'X', 28 <AR12>
R:Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
EMBO J. 7, 675-680, 1982
A:Title: Two yeast acid phosphatase structural genes are the result of a tandem duplicat
A:Reference number: S41855; MUID:84236032; PMID:6329697
A:Accession: S41855
A:Molecule type: DNA
A:Residues: 1-30, 'T', 32-51, 'S', 53-75 <MEY>
A:Cross-references: EMBL:M24178; NID:9172156; PIDD:AAA34858.1; PIDD:9172157
R:Tait-Kamrad, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G
Mol. Cell. Biol. 6, 1895-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A:Reference number: A93074; MUID:87064474; PMID:3537710
A:Accession: B25241
A:Molecule type: DNA
A:Residues: 1-44 <TAI>
R:Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A:Title: A DNA fragment containing the upstream activator sequence determines nucleoscm
A:Reference number: A25367; MUID:67564556; PMID:3023327
A:Accession: A25367
A:Molecule type: DNA
A:Residues: 1-2, 'Y', 4-43, 'T', 45-51 <BER>
R:Silve, S.; Monod, M.; Hinnen, A.; Hagenauer-Tsapis, R.
Mol. Cell. Biol. 7, 3366-3314, 1987
A:Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin

A:Reference number: A27774; MUID:88039886; PMID:3313013
A:Accession: A27774
A:Molecule type: DNA
A:Residues: 1-51, 'S', 53-60 <SL>
A:Cross-references: GB:X17306
C:Genetics:
A:Gene: SGD:PHO5; MIPS:YBR093C
A:Cross-references: SGD:S0000297; MIPS:YBR093C
A:Map position: 2R
A:Note: YBR093C
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hyd
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-467/Product: acid phosphatase, repressible #status experimental <MAN>
F:75/Active site: His [phosphohistidine intermediate] #status predicted
F:97,123,162,192,250,315,356,390,439,445,456,461/Binding site: carboxylate Asp; co
F:337/Active site: His #status predicted

Query Match 16.5%; Score 385; DB 1; Length 467;
Best Local Similarity 26.2%; Pred. NC. 1.9e-20;
Matches 14; Conservative 66; Mismatches 159; Indels 66; Gaps 14;

QY 26 GOVAPFFS-ANRESV-SPEVPAGCRVTFACVLGRHGAARYPTDSKGRKYSALIEBIOQNAVTT 85
DB 42 GGAGPYYSFGDYGISRDLPCEGCEMQLQWVGHRGERTVTS-AKTIKSTWYKLSNVTRQ 101
QY 86 FCGKAPFJK-TYNYSLGAD- - - - -LTPF-GEQELVNSG-KFYGRYSLSJR 129
DB 102 FNGSLFLANDDYEFFIRDDDDLEMETTFANSDVDLNPYTCEXNAKSHARDFLACYGYMVE 161
QY 130 NIYPFF-IRSSGSRV-ASGKKE-EGFQSL-KLXDPRAQCGOSSPKLDVISEASSSNTLD 184
DB 162 NOTSFVFTSNKRCHDTAQYFDG- - - - -LGD- - - - -OFNITLCTVSEAESAGANTLS 210
QY 199 P-GTCTVFEDSELADTVEANFTATPVPS-RQRJENDLSGVLTDTETVTVXNDKCSFDTIS 247
DB 21: ACKSCPAW-DYDANDQVNEVDYTYLDD-AKR-LNKENKG-NLTSTCASTLFSKCAFE- - - 266
QY 248 TSTVUTK-LSPFCOLTHWEKINVDYQLSKKYGHGAGNPLGPTCGVYANELLARLTH 306
DB 247 --VNAGYSVDGDIPTKDELVHYSYVDLHTYHEGPGYDI-KSVGSSNLFNASVKKLKQ 323
QY 307 SPVHDDTSSNHLDDSPATFPLNSTLYADPSHDNGHISILFALGLYNGTKPKPTTTVENI 366
DB 324 SEIQD- - - - -QKWLSTFHTD-LNFTJTAGIIDDKNKJFAEVVPM 365
QY 367 TQDGFSSAKTVPFASRLYVEMQCAEQEPLRVLVNDRWVFLHGPVDAIGRTRDSF 426
DB 366 GNT--FRRSWYVPGARVYVTEKFOC--SNCTYVRYVINDAVVP-ETCSTGPGFSCEINOF 421
QY 427 - - - - -VRGLSPAR 434
DB 422 YDYAEKRVAGTDFLK 436

RESULT 5

PABVCC
acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092C
C:Species: *Saccharomyces cerevisiae*
C>Date: 30-Sep-1991 #sequence revision 09-Sep-1994 #text change 05-Nov-1999
A:Accession: S48259; S45960; S05794; A25241; S44674
R:Mannhaupt, G.; Stucka, R.; Ehle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A:Reference number: S48255; MUID:95208357; PMID:7900426
A:Accession: S48259
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-467 <MAN>
A:Cross-references: EMBL:X78993; NID:9476045; PIDD:CAA55597.1; PIDD:9476050
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R:Feldmann, H.; Mannhaupt, G.; Schwarziolse, C.; Vetter, I.

submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927

A:Accession: S45960

A:Molecule type: DNA

A:Residues: 1-467 <PE2>

A:Cross-references: EMBL:Z35961; NID:G516362; PIDN:CAA85245.1; PID:G516363; GSPDB:GN5000

R:Baiba, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.

Nucleic Acids Res. 22, 7721-7739, 1994

A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast

A:Reference number: S45794; MUID:8503794c; PMID:6053051

A:Accession: S45794

A:Molecule type: DNA

A:Residues: 1-218, 'MAJ1', 222-467 <BAJ1>

A:Cross-references: EMBL:X01080; NID:G4148; PIDN:CAA25557.1; PID:3759281

A:Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue

R:Rait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, G.D.; Scsian, S.J.; Thill, G.

Mol. Cell. Biol. 6, 1855-1865, 1986

A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within

A:Reference number: A93074; MUID:87064474; PMID:3537710

A:Accession: A25241

A:Molecule type: DNA

A:Residues: 1-44 <TAI>

C:Genetics:

A:Gene: SGD:PHO3; MFS:YBR092C

A:Cross-references: SGD:SC000236; MIPS:YBR092C

A:Map position: 2R

C:Superfamily: Yeast acid phosphatase

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-467/Product: acid phosphatase, constitutive #status predicted <ANT>

F:75/Active site: His (phosphatidyl intermediate) #status predicted

F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval

F:337/Active site: His #status predicted

Query Match 16 58; Score 385; DB 1; Length 467;

Best Local Similarity 26.18; Pred. No. 1.9e-20;

Matches 113; Conservative 63; Mismatches 195; Indels 62; Gaps 11;

Qy

26 GQYAPFFSLANESV:SPVPAGCRVTFQVLSRHGARYPTDSKGRKYSALIEIQNATT 65

Db

42 GGAGPYSPFCGYC:SRCLPEGCCKQLQMLARGERYP:YSGATIMTKWYKLSNTRQ 101

Qy

86 FDGYAFILK-TYNSLGADD-----LTFP-GEQLVNSGKIFQRIEJSTR 129

Db

102 FNGSLFUNDYEFIRDDOLEMETTANSNDVNPYTGEMAKAHAREFLAQGYMFE 161

Qy

130 NIVPF-IRSSGSRVIAAGKAFIEGFCSTKLKOPRAQPGQSSPKIDVY-SEASSNLTLD 186

Db

162 NQTSFP-FAASSRVHOTAQYFDG-----LGD-----GFNISLQTVSEAMGAGANTLS 210

Qy

189 PGTCTVPEDSELADTVEANFTATVPISIRGRLNENLDSGLVTLTTEVTYIMDKCSPTIST 248

Db

211 AGNACPGKCEANDDILCKYDTYLDJIAKRLKKNKGNLTSCANTLFAWCAVEANAR 270

Qy

249 STVDTKLSPFDLTFHDEW:NVQYLSKLYYGHGAGNP:SGTQGYGANELLARIITSP 308

Db

271 GYSDV-----CDITFEDELNRYSGQLVSPYQDGPYDMIRSVGANL:FNATLKLKQSE 325

Qy

309 VHDUTSSNHT:DCSPATFPLNST:YADPFSHNGI:SIILFALGLYNGTKPLSTTTTIV 368

Db

326 TQC-----LKNVLSFTHTDILNLTTLTAT:IDCKKNLTABYVVPFMGN 367

Qy

369 TDGFSAMTVPFASRLYYVMQCAEQEP:LVRLVNDVRVPLHSCPYDALGRCTRDSF-- 426

Db

368 T--FKKSYVVGARVYTEKFQC--SNDTYRVYVINAVVPIETCT:GPGFSCE:INDFD 423

Qy

427 -----VRGLSFAR 434

Db

424 YAEKRVAGTDFLK 436

RESULT 6

S52495

RESULT 7

S53476

acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YAR071w

C:Species: Saccharomyces cerevisiae

C:Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000

C:Accession: S53476; JCI018

R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; K

acid phosphatase homolog YDLO24c - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein D2815

C:Species: Saccharomyces cerevisiae

C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 19-Apr-2002

C:Accession: S52495; S67556

R:Andre, B.; Visser, S.; Jurestarazu, L.

submitted to the EMBL Data Library, February 1995

A:Description: The sequence of a 42 kb segment located on the left arm of chromosome

A:Reference number: S52492

A:Accession: S52495

A:Molecule type: DNA

A:Residues: 1-468 <AND>

A:Cross-references: EMBL:Z48432; NID:G683669; PIDN:CAA89335.1; PID:G683673

A:Experimental source: strain S288C

R:Jurestarazu, L.A.; Andre, B.; Visser, S.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67535

A:Accession: S67556

A:Molecule type: DNA

A:Residues: 1-468 <URR>

A:Cross-references: EMBL:Z74072; NID:G1430996; PIDN:CAA98503.1; PID:G1430997; MIPS:YD

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:DIA3

A:Cross-references: SGD:SC002182

A:Map position: 4L

C:Superfamily: yeast acid phosphatase

Query Match 15 8; Score 368; DB 2; Length 468;

Best Local Similarity 25.6; Pred. No. 3.4e-19;

Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;

Qy

26 GQYAPFFSLANESV:SPVPAGCRVTFQVLSRHGARYPTDSKGRKYSALIEIQNATT 85

Db

43 GGSAPYSPFANVGIPTDPEGCRLTQVQMICRHERYPTREAKDIFEWYKISNYTKG 102

Qy

86 FDGYAFILK-TYNSL-----GADDLTFP-GEQLVNSGKIFQRIEJSTR 129

Db

103 YEGSLFPLNGYEFF-PDESLLMETTLQNS:DLVNPYTGEMAKAHAREFLAQYKLMLE 162

Qy

130 NIVPF-IRSSGSRVIAAGKAFIEGFCSTKLKOPRAQPGQSSPKIDVY-SEASSNLTLD 184

Db

163 NC:NFPITFINSKRIYDTACYPALALGDGFNIS-----LQTLSENSSSGA 207

Qy

185 NTLOPGTCTVFEDSELA:CTVEANFTATVPISIRGRLNENLDSGLVTLTTEVTYIMDKCSPT 244

Db

208 NTLAAKSCPMWASNNNDILXYSRDY:LENISDRUNDENKGLNLSRKDAALFNSWCAFE 267

Qy

245 TISTSTVDTK-LGSPFCDLTFHDEW:NVQYLSKLYYGHGAGNP:SGTQGYGANELLARI 303

Db

268 -----LNAGYSNICDIFSAELIHYSVETDLTSTFYQNGPGYKLIK:GANL:FNATV-K 320

Qy

304 LTHSPVHDDTSSKNTLDSPPATFPLNSTLYADPFSHNGI:SIILFALGLYNGTKPLSTTTIV 363

Db

321 LIROSAS-----LQKWLSTHTDILNLTTLTATG:LDTRNCTTNHV 363

Qy

364 ENITQTDGFSAMTVPFASRLYYVMQCAEQEP:LVRLVNDVRVPLHSCPYDALGRCTR 423

Db

364 P--FRCHSYRHSYVPGGARVYTEKFQC--SNDTYRVYVINAVVPIESCSGPGFSCEE 419

Qy

424 DSF-----VRGLSF 432

Db

420 GTFVEYAKDRILRGVSF 435

submitted to the EMBL Data Library, February 1994

A:Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the
A:Reference number: S53458
A:Accession: S53476
A:Molecule type: DNA
A:Residues: 1-467 <BUS>
A:Cross-references: EMBL:J28920; NID:91616966; PIDN:AAC9503.1; PID:9456155; MIPS:YAR071
R:Chen, J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A:Title: The primary structure of acid phosphatase gene PHO11 in *S. cerevisiae* and compa
A:Reference number: JCI018
A:Accession: JCI018
A:Molecule type: DNA
A:Residues: 1-16, 'J', 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 <CHE>
A:Note: this paper is in Chinese, with an English abstract
C:Genetics:
A:Gene: SGD:PHO1
A:Cross-references: SGD:SC000094; MIPS:YAR071W
A:Map position: 1R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester; hydroly

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase #status predicted <Mat>
F:74/Active site: Arg #status predicted
F:75/Active site: His (phosphohistidine intermediate) #status predicted
F:37,462,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 15.1% Score 352; DB 2; Length 467;

Best Local Similarity 24.4%; Pred. No. 5.1e-18;

Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 26 GCYAPFESLANESVSPVAGCEVTFQAQVSRHGARYPTDSKGYKYSALIEIQNATT 85
DB 42 GSGPYYSFGDYGISRDLPESCCEMKQVQVGRHGERYPTVSKAKSMTTWYKLSNVTGQ 101
QY 86 FCGKYAFK-----TNYNS-----GADLTFF-GEQELVNSGIRFYQRYESLTR 129
DB :02 FSGALSFLNDYEFFRDTKYLEMETTLANSVNVNLFYTGEMNAKRHARDFLAQYGYWE 161
QY :30 NIVVF--RSGSSRVASGKKFEGFQSTLKDPRAQCGSSPKIDV---VSEASSN- 194
DB 162 NQTSFAVFTSNRCHDTAQVFDGL-----GSKFNISLQTSEASAGA 206
QY :85 NTLDP-GTCTVEDSLATVEANFTATVPFSIRQRLNDLSGVLTDTTEVYLMDCSF 243
DB 207 NTLAHSHPAMDG--GVNDIDILKKYDTRKYLGLAKRLNKGJLNTSSDANTFFAMCAY 265
QY 244 DTISTSTVDTKLSFFCCLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELIAR 303
DB 266 EINARG-----YSDICNIFTKDELVRFSYQDLETTYQTGPGYDVVRSGANLFNASVKL 320
QY 304 JTHSPVHDTSSNHTLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLSTTTV 363
DB 321 LKSEVQD-----QKWLSTHDTDLNLTITIGIIDCKNNLTAEHV 362

QY 364 ENITQTGGSSAMTVFPASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPCVDALGRCTR 423
DB 363 PMENT--FHRSWYVQGARVYTEKFC--SNDTYVRVINDAVVPIETCTSTGPGFSCEI 419
QY 424 DSF-----VRGLSPAR 434
DB 419 NDFYGYAEKRVAGCTDFLK 436

RESULT 8
S48996
acid phosphatase (EC 3.1.3.2) PHO12 - yeast (*Saccharomyces cerevisiae*;
N:Alternate names: protein YHR215W
C:Species: *Saccharomyces cerevisiae*
C:Date: 02-Dec-1994 #sequence_revision: 02-Dec-1994 #text_change 22-Jun-1999
R:Macri, C.
submitted to the EMBL Data Library, February 1994

A:Description: The sequence of *S. cerevisiae* cosmid 9.77.

A:Reference number: S46671
A:Accession: S48996
A:Molecule type: DNA
A:Residues: 1-467 <MAC>
A:Cross-references: EMBL:U00029; NID:9551322; PIDN:AAB69729.1; PID:9458917; MIPS:YHR21
R:Xi, L.
submitted to the EMBL Data Library, January 1995
A:Reference number: S59658
A:Accession: S59659
A:Molecule type: DNA
A:Residues: 1-16, 'J', 18-81, 'AR', 84-149, 'H', 151-467 <XUL>
A:Cross-references: EMBL:J19789; NID:9847754; PIDN:AAA73479.1; PID:98647755
C:Genetics:
A:Gene: SGD:PHO12
A:Cross-references: SGD:SC001258; MIPS:YHR215W
A:Map position: 8R
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 15.1% Score 352; DB 2; Length 467;

Best Local Similarity 24.4%; Pred. No. 5.1e-18;

Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 26 GCYAPFESLANESVSPVAGCEVTFQAQVSRHGARYPTDSKGYKYSALIEIQNATT 85
DB 42 GSGPYYSFGDYGISRDLPESCCEMKQVQVGRHGERYPTVSKAKSMTTWYKLSNVTGQ 101
QY 86 FCGKYAFK-----TNYNS-----GADLTFF-GEQELVNSGIRFYQRYESLTR 129
DB :02 FSGALSFLNDYEFFRDTKYLEMETTLANSVNVNLFYTGEMNAKRHARDFLAQYGYWE 161
QY :30 NIVVF--RSGSSRVASGKKFEGFQSTLKDPRAQCGSSPKIDV---VSEASSN- 184
DB 162 NQTSFAVFTSNRCHDTAQVFDGL-----GSKFNISLQTSEASAGA 206
QY :85 NTLDP-GTCTVEDSLATVEANFTATVPFSIRQRLNDLSGVLTDTTEVYLMDCSF 243
DB 207 NTLAHSHPAMDG--GVNDIDILKKYDTRKYLGLAKRLNKGJLNTSSDANTFFAMCAY 265
QY 244 DTISTSTVDTKLSFFCCLFTHDEWINDYLSLKYKYGAGNPLGPTQGVYANELIAR 303
DB 266 EINARG-----YSDICNIFTKDELVRFSYQDLETTYQTGPGYDVVRSGANLFNASVKL 320
QY 304 JTHSPVHDTSSNHTLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLSTTTV 363
DB 321 LKSEVQD-----QKWLSTHDTDLNLTITIGIIDCKNNLTAEHV 362
QY 364 ENITQTGGSSAMTVFPASRLYVEMMQCAEQEPPLVRVLVNDRVVPLHGCPCVDALGRCTR 423
DB 363 PMENT--FHRSWYVQGARVYTEKFC--SNDTYVRVINDAVVPIETCTSTGPGFSCEI 419
QY 424 DSF-----VRGLSPAR 434
DB 419 NDFYGYAEKRVAGCTDFLK 436

RESULT 9

UN0715

3-phytase (EC 3.1.3.8) B precursor - *Aspergillus ficuum*

N:Alternate names: pH 2.5-optimum acid phosphatase

C:Species: *Aspergillus ficuum*

C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999

C:Accession: UN0715; P00594; P00460

R:Enrich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.

Biochem. Biophys. Res. Commun. 195, 53-57, 1993

A:Title: Identification and cloning of a second phytase gene (phyB) from *Aspergillus n*:

A:Reference number: UN0715; MUID:93371452; PMID:7916610

A:Accession: UN0715

A:Molecule type: DNA

A:Residues: 1-479 <ERR>

A:Cross-references: GB:L20567

A:Accession: P00594

A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <EH2>
R:Ullah, A.H.J.; Dischinger Jr., H.C.
B:Chem. Biophys. Res. Commun. 192, 754-759, 1993
A:Title: Identification of active-site residues in *Aspergillus ficuum* extracellular pH 2
A:Reference number: P00460; MUID:92249452; PMID:8484781
A:Accession: P00460
A:Molecule type: protein
A:Residues: 65-66;68-93 <ULL>
C:Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.1.3.2), hy
C:Genetics:
A:Gene: phvB
A:Introns: 261/1; 300/2; 335/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-479/Product: 3-phytase #status experimental <MAT>
F:81.337/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted
F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu
Query Match 14.4%; Score 337.5; DB 1; Length 479;
Best Local Similarity 27.9%; Pred. No. 6.1e-17;
Matches 109; Conservative 59; Mismatches 166; Indels 57; Gaps 15;
QY 40 ISPEVPAGCRVTFACVLSRHRGARYPTDSKGKKY-SALIEEQONATTPDGKVAFLKTYNY 98
DB 63 IARDPTGCEVDQVYMKRHRGERYSPSACKSIEELAKVYSINTTEYKGLDLAFNDWTY 122
QY 99 SL-----GADLT-PP-GEQELVNSGKIFYORYESL--TRNIVPPIRSSGSRVIAAGK 148
DB 123 YVPNECYNAETISQPYAGLLDAYNHGNDYKARYGHLWNGETVVPFF-SSGGRVIETAR 181
QY 149 KFIQFQSTKLKOPRAQGGSSPKIDVISEASSNNITLDPGCTVFEDSELAOTVEANF 208
DB 182 KFGEGFGYNY-----STNAALNIISESEVWGASLTP-TCDDNDQTTCDNLTYQL 232
QY 209 TATFVPSIRQRLNDLSGVLTDETVYLMDCSFDTSTSTVTKLSPPFCDLTHDEWI 268
DB 233 PCFKVAARLNSQN--PGMNLTASDVYNYMASFELNA-----RPFKNWNAFTQCEWV 285
QY 269 NYDYLOSLKXYGHGAGNPLGPTGGVYANELLARLTHSPVHDDTSSNHTLDSPPATPPL 328
DB 286 SFGYVEDLNYCYACGPGDKMAAGVAYANASLTLLNQGP-----KQAGP----- 330
QY 329 NSTYAFDFSHNGISILFAGLY--NGTKPLSTTTVENITQDGFSSAMTVFPASRLYV 386
DB 331 ---LFFNLADHTNITPILALGVLPNEDFLDRAVAGN-----PYSIGNVPMVGGHJTI 382
QY 387 EMWQCCA-----EQEPLRVLVNDRVVPLHGC 413
DB 383 ERLSCOTALSDKSTYVLVYNEAVLPFNDG 413
RESULT 10
JC42890
acid phosphatase (EC 3.1.1.3.2) precursor - *Aspergillus awamori*
C:Species: *Aspergillus awamori*
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 1-1-Jun-1999
C:Accession: J042890
R:Riddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; M
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
A:Reference number: J042890; MUID:94040796; PMID:8224894
A:Accession: J042890
A:Molecule type: DNA
A:Residues: 1-479 <PID>
A:Cross-references: GB:L02420; NID:G166481; PIDN:AAA:6897.1; PID:G166482
A:Experimental source: strain ALK0243
C:Comment: The highly similar enzyme from *A. ficuum* has been shown to have 3-phytase (EC
C:Genetics:
A:Gene: aph
A:Introns: 261/1; 300/2; 335/2

C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phos
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-479/Product: 3-phytase #status predicted <MAT>
F:81.337/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted
F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #stat
Query Match 14.4%; Score 336.5; DB 1; Length 479;
Best Local Similarity 27.6%; Pred. No. 7.2e-17;
Matches 108; Conservative 58; Mismatches 168; Indels 57; Gaps 14;
QY 40 ISPEVPAGCRVTFACVLSRHRGARYPTDSKGKKY-SALIEEQONATTPDGKVAFLKTYNY 98
DB 63 IARDPTGCEVDQVYMKRHRGERYSPSACKSIEELAKVYSINTTEYKGLDLAFNDWTY 122
QY 99 SL-----GADLT-PP-GEQELVNSGKIFYORYESL--TRNIVPPIRSSGSRVIAAGK 148
DB 123 YVPNECYNAETISQPYAGLLDAYNHGNDYKARYGHLWNGETVVPFF-SSGGRVIETAR 181
QY 149 KFIQFQSTKLKOPRAQGGSSPKIDVISEASSNNITLDPGCTVFEDSELAOTVEANF 208
DB 182 KFGEGFGYNY-----STNAALNIISESEVWGASLTP-TCDDNDQTTCDNLTYQL 232
QY 209 TATFVPSIRQRLNDLSGVLTDETVYLMDCSFDTSTSTVTKLSPPFCDLTHDEWI 268
DB 233 PCFKVAARLNSQN--PGMNLTASDVYNYMASFELNA-----RPFKNWNAFTQCEWV 285
QY 269 NYDYLOSLKXYGHGAGNPLGPTGGVYANELLARLTHSPVHDDTSSNHTLDSPPATPPL 328
DB 286 SFGYVEDLNYCYACGPGDKMAAGVAYANASLTLLNQGP-----KQAGP----- 330
QY 329 NSTYAFDFSHNGISILFAGLY--NGTKPLSTTTVENITQDGFSSAMTVFPASRLYV 386
DB 331 ---LFFNLADHTNITPILALGVLPNEDFLDRAVAGN-----PYSIGNVPMVGGHJTI 382
QY 387 EMWQCCA-----EQEPLRVLVNDRVVPLHGC 413
DB 383 ERLSCOTALSDKSTYVLVYNEAVLPFNDG 413
RESULT 11
JC4285
acid phosphatase (EC 3.1.1.3.2) precursor - yeast (*Pichia pastoris*)
N:Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C:Species: *Pichia pastoris*
C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
C:Accession: J04285
R:Payne, W.E.; Gannor, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A:Title: An inducible acid phosphatase from the yeast *Pichia pastoris*: Characteriza
A:Reference number: J04285; MUID:96001238; PMID:7557473
A:Accession: J04285
A:Molecule type: DNA
A:Residues: 1-468 <PAY>
A:Cross-references: GB:U28658; NID:G881955; PIDN:AAA85503.1; PID:G881955
A:Experimental source: GS:15
C:Genetics:
A:Gene: pho1
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hyd
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-468/Product: acid phosphatase #status predicted <MAT>
F:84/Active site: His (phosphohistidine intermediate) #status predicted
F:83,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predic
F:345/Active site: His #status predicted
Query Match 14.0%; Score 327; DB 2; Length 468;
Best Local Similarity 25.1%; Pred. No. 3.4e-16;
Matches 112; Conservative 65; Mismatches 178; Indels 92; Gaps 17;
QY 25 WQYAPFFSLANESVISPEVPAGCRVTFACVLSRHRGARYPTDSKGKYSALIEE-IQNA 83

```
Db 62 WG-----IAEAEIE-----SCTDQAHLLVRHGERYFSTNVGQLEALYKQLDADV 109
QY 84 TTFDGKFAFKTNYSIGADELTPFGQELVNS-----GKFKYQRYESLNRNV 132
Db 110 EVPTGPLSPFDQDYFYSD---AAWYEQETTKGFYSGNLNADFPGTTLRERYDHLNISE 166
QY 133 P-----FIRSSGSRVIASGKKFIEGPOSTKLEKPRAPGQSSKIDVWISSEASS-----NN 185
Db 167 EKKLSWAGSQERVDVTAIFYAGFMKSNYTS-----MVEVLAEEKSOGLNS 216
QY 186 TLDPGTCT-----VFDESELADTV---EAFNATFVPSIRORLENDLSGVLTDTTEVYL 237
Db 217 LTARISCPNYSNHYKDGDFNDPNDIAERADRLNLSLSP-----GFNITADIP-- 265
QY 238 YDMCSPFTTISTVDTKLSFPCFLTHDEMINVDYQSLKKYKYGAGNPLGPTQGVYA 297
Db 266 ALXCGFELNVRGE-----SSFCVDLREALLYAYLRDLGWYVNGVGNPLGKTIGWYA 320
QY 298 NELIARJTHSPVHDTSSNHTLSSPATFPLNLTLYADESHDNGIISILFALGLYNGTK- 356
Db 321 NATROLLENT-----EADPRDYP---LYFSHDTLLQVFTSLGLFRVTSJ 364
QY 357 FLSTTTVENTTQDGFSSAKTVFPFASRLYVEMQCC--QAEQEPLRVLRVNDVRVVP- 414
Db 365 PL-----DQIQFCTSPKSTEIVPMGARLLTERLLCTVEGEKYVYVRTLNDVFP- 419
QY 415 VDALGRCTRDSFVRGLSFARSGSDNAE 441
Db 420 SGFGFCPCPNVYSRUEALNEDSDFAE 446

RESULT 12
T39929
Chitin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 53-Dec-1999 #text_change 21-Jan-2000
C:Accession: T39929
Ri:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21857
A:Accession: T39929
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-463 <LYN>
A:Cross-references: EMBL:AA023286; PIDN:CAAI1863.1; GSPDB:GN00067; SPDB:SPB22LH7.03c
A:Experimental source: strain 972h-; cosmid c2.117
C:Genetics:
A:Gene: SPDB:SPB22LH7.03c
A:Map position: 2
C:Superfamily: yeast acid phosphatase

Query March 12.9%; Score 296.5; DB 2; Length 463;
Best Local Similarity 26.4%; Pred. No. 3.2e-14;
Matches 108; Conservative 61; Mismatches 180; Indels 60; Gaps 14;

QY 28 YAPFFSLANESVTSPEVACRVTFAQVLSRHRGARYP-----TDSKGGKYSALTEE--- 78
Db 43 HEYFP-----DGLDSAFPETCEQQVHLQRHRSNPTGDVTA:DVYSQYLNNGEKLL 97
QY 79 ---TQNATTFDGKFAFLKTYNYSL---GADDLTPFGEQELVNSGKFKYQRYESLNRNV 132
Db 98 NGSPVNFYSVPENPCFKQWTEPVIDAENADQLSSRGRLEFLDLGRQLCYRYVKLPFSYV 157
QY 133 PFRSSGSRVIASGKKFIEGPOSTKLEKPRAPGQSSKIDVWISSEASSNNITLDP 189
Db 158 YDINTAEQERWESAKFTYGVGDKRNYE-----KTNFILISEGKAAGANSLSMY 207
QY 190 GTCTVFEDSEL-----ADTVENATFATFVPSIRORLENDL-SGVTLDTTEVYMDMCSFD 244
Db 208 NACPVFKDNFNKNTADAAHVRN:FIEPIVNRKAYFDSSVKLTINDVRSIFYTCEYE 267
QY 245 TISTSTVDTKLSFPCDLTHDEMINVDYQSLKKYKYGAGNPLGPTQGVYANEIARL 304
```

```
Db 268 IAKCHSD-----FCSITPSEFLNFYDSLDGAYGGPVSEWASTJGGAYINKLA--- 319
QY 305 THSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGKIISILFALGLYNGTKPLSTTIVE 364
Db 320 -----DSLRYNT---NP---DFDRKVP-LAFTHDSNLIIPVEAALGFFFDITPQNPPLTD 366
QY 365 NTQDGFSSAWTVFPFASRLYVEMQCCQAEPLRVLRVNDVRVPLHGC 413
Db 367 KNIYTSOKTSFPFAGNLITELFFC-SDSKYYVRHLNVQVYPLIDC 414

RESULT 13
A25326
acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharon
C:Species: Schizosaccharomyces pombe
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A25326; T50435
R:Elliot, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J.
J. Biol. Chem. 267, 2936-2941, 1996
A:Title: Isolation and characterization of the structural gene for secreted acid phos
A:Reference number: A25326; MUID:8614050; PMID:305272
A:Accession: A25326
A:Molecule type: DNA
A:Residues: 1-453 <ELL>
A:Cross-references: GB:M11857; NID:G173422; PIDN:AAA3321.1; PID:G173423
R:Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25068
A:Accession: T50435
A:Molecule type: DNA
A:Residues: 1-453 <R13>
A:Cross-references: EMBL:AL137099; PIDN:CA86657.1; GSPDB:GN00067; SPDB:SPBFA63.12
A:Experimental source: strain 972h(-); clone pl p4G3
C:Genetics:
A:Gene: PHO1; SPDB:SPB24G3.02
A:Map position: 2
C:Superfamily: Yeast acid phosphatase
C:Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F.69/Active site: Arg #status predicted
F.69/Active site: His (phosphohistidine intermediate) #status predicted

Query March 12.7%; Score 296.5; DB 1; Length 453;
Best Local Similarity 24.5%; Pred. No. 5.6e-14;
Matches 103; Conservative 57; Mismatches 190; Indels 71; Gaps 12;

QY 18 PSETSHLWQ---YAPFFSLANESVISPEV--PACRVTFAQVLSRHRGARYPTDSKGGKY 72
Db 30 PDFXHLTSRSFYHKPYF-----YGPSIDFPPTCKIKQVHT-QRHGSRNPTGGNAFD 82
QY 73 SALIEEQ-----NATTFDGKFAFLKTYN---YSLGADDLTPFGQELVNSGKIF 120
Db 93 AVGIANFOORLLNGSVPIDYSVSGNPLSPVPTPTVTEANADALSSSRVELFDMGRQF 142
QY 121 YCRYESLNRNVTPFIRSSGSRVIASGKKF-----IEGQSTKLKDPRAQPGQSSPK 172
Db 143 YERYHELFNASTYNIYTAQQRVVVDSALWYGYGFGEDVHNFTNY1LVSENAAGNS-- 200
QY 173 IDVVISASSNNLTDPGCTCTVFEDSELACTVEANFTATFVPSIRORLENDLSGVLTDT 232
Db 201 -----LSSYN-----ACPSADADDFTTAPAEARNVYMPPTQRNLNPFYSNYLTND 247
QY 233 EYVTLMDMCSFDTISTTSTVDTKLSFPCDLTHDEMINVDYQSLKKYKYGAGNPLGPTQ 292
Db 248 DILNLYGICSEIALQD-----YSEFKLFNSVDLFNEFEGDLSFSGMNSVKWGSIF 302
QY 293 GVGVANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLY 352
Db 303 GGAYANSLANSLR-----SVENNT-----QQVFFAFTHDANILPVEALGFF 344
QY 353 NGTQPLSTTIVENTTQDGFSSAWTVFPFASRLYVEMQCCQAEPLRVLRVNDVRVPLH 412
Db 345 TDNTPENPLPTSYOVHSHSKASEFVPFAGNLTELFOCE-DSKYYVRHLNVNEEVPFLSD 403
```

QY 413 C 413

Db 404 C 404

RESULT 14

S14119
acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1993
C:Accession: S14119; T45455
R:Yang, C.; Schweingruber, X.E.
Curr. Genet. 18, 269-272, 1990

A:Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe
A:Reference number: S14119; XUID:51064763; PMID:2249257
A:Accession: S14119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <YAN>
A:Cross-references: GB:X56939; NID:G5006; PIDN:CAA40258.1; PID:G5007
R:Lyne, M.; Rajandream, M.A.; Barré, B.G.; Baker, S.; Murgall, K.
submitted to the EMBL Data Library, November 1998

A:Reference number: Z21931
A:Accession: T40455
A:Status: preliminary; translated from GB/EMBL/CDDB3
A:Molecule type: DNA
A:Residues: 1-463 <LYN>
A:Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GNC0067; SPDB:SPBC428.03C
A:Experimental source: strain 972h-; cosmid c428
C:Genetics:
A:Gene: SPBC428.03C
A:Map position: 2
A:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 12.28; Score 284; DB 2; Length 463;
Best Local Similarity 24.98; Pred No. 4.8e-13;
Matches 102; Conservative 66; Mismatches 181; Indels 60; Gaps 13;

QY 28 YAPFSSANESVISPEVACGRVTFQVLSRHGARYP-----TDSKGGKYSALIE---- 77

Db 43 HEVFNQPTTS-----FPESCAIKQVHLQKHGSRNPTGDDTATDVSSAQYIDIFQNKLL 97

QY 78 --EIQQNAITFDGKAYALKYNSL-----GADLLTPGCEELVNSGKFKYQRYESLIRNIV 132

Db 98 NGSTPVPKFSVPENPYFKKATVPVKAENADQSSGRLEIFDLGRQVFRYELFTDQV 157

QY 133 PFIRSSGSRVIASSKKFIEGFQSTKLKDFRAQFGSSPKIDVY---SEASSNNTLP 189

Db 159 YDINTAAQERVDSAEWFSYGMPCDDQN-----KTNFIVLPEDESAGANSLAY 207

QY 190 GTCVTFEDSELADTVANETA---TFVPSRQLENDL-SGVTLTETEVYINEXGSTD 244

Db 208 YSCPYEDNNIDENITFAAHTSMRNVPKPIANRLAKYFDSGYNLTVDSYRSLVYCYVE 267

QY 245 TISTSTVDTKLSPPCDLFTDWINVYLOSKKYCHGAGNPLGPTQGVYANEZAKL 304

Db 268 IALRQNSD-----FCSLFTSEFNFYDSDLDVAYWGGPASEWASTLGGAYNNLANL 322

QY 305 THSPVHDDTSNHFIDSSPAPFPANSTLYACFSDHNGIISLPALGLYNTKPKLSITTTVE 364

Db 323 R-----KGVNNSADRK-----VPLAF-HDSQIPVEAALGFFPDITPERPLPTD 366

QY 365 NITDGFSSAWTPFASRLVYEMMQCAQCEQLVRYVANDRVVPLHGQ 413

Db 367 KNIFTYLSKTSFVFFAGNLITELFLC-SKNKYVRELVNQVYPLTDC 414

RESULT 15

A86233

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001

C:Accession: A86233

R:Theologis, A.; Ecker, C.R.; Pain, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Atton
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, C.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, C.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kit,
C.A.; Li, S.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc
ker, M.; Wu, J.; Yu, G.; Fraser, C.M.; Vetter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosomes 1 of the plant Arabidopsis.

A:Reference number: A86.41; MJD:2016719; PMID:11130712

C:Accession: A86233

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-468 <STC>

A:Cross-references: GB:A8005172; NID:G216077; PIDN:AAB60742.1; GSPDB:GN00141

C:Genetics:

A:Map position: 2

C:Superfamily: yeast acid phosphatase

Query Match 6.38; Score 148; DB 2; Length 468;
Best Local Similarity 21.88; Pred No. 0.0044;
Matches 100; Conservative 60; Mismatches 202; Indels 96; Gaps 13;

QY 11 VDQYQCFSEISHL--WGQYAPFSSANESVISPEVACGRVTFQVLSRHGARYPT--- 65

Db 16 VSQADQGFVDRHRLSTVTRYSTKDVTONLIESKNVSECTPIHLNLVARHGTRSPTKR 75

QY 66 ----DSKGGKYSALIEIQQNAITFDGKAYFL---KTYNSLGADLLTPPGCEELVNSG 117

Db 76 LRELSIAGRFKELVRDAEARKLPSKIPGKIQWKSFWGKVKGGELIRQGCDELVQLG 135

QY 118 IKFYQRYESLIRN-----IVPFIRSSGSRVIASSKKFIEGFQSTKLKDFRAQFGSSPKI 173

Db 136 IRVTERFPLSPERDYPHDVVTIRATQIPRASASAVAFGMSLFSEK---GNLGFGRN--RA 183

QY 174 DVVISEASSNNLDPGCTCTVFEDS-----ELADTVANFTATFVPSIRQLEND 223

Db 191 FAVTSENKRASDTKLRFEECCQNYKSYRKAKEPAVDKLEPVLNKKTA-----SVAKRYD-- 244

QY 224 LSGVTLTDTETVYXDMCSFDTTISTVDTKLSPFCDLFTDWINVYDYLQSLKKYVGHG 283

Db 245 ---LKFTKQDISLWFLCKQVALL-----EMTD-----DSEVELLKG 278

QY 284 AGNPLGPTQGVYANELIARLTHSPVHDDT--SSNHTLDSSPATFPANSTLYA--DFSHD 339

Db 279 YGNSJANYKMGV-----PLLEDVLSMEEAIKAREEKLPPGSGYEKARLRFAPA 325

QY 340 NGIISILFALGLY-NGT-----KPLSTTTVENITCTDGFSSAWTPFASRLVYEMMQ 390

Db 326 ETTPVPSCLGLGFCDGSEFEKIOKEKLELF--PQPKTRDFRGSNAPFGGNNILVLYS 383

QY 391 CCAEQEP--LVRYVANDRVVPLHGCPVDALGRCTTDSF 426

Db 384 CPAESSPKYFVQLHNEHP-APVGC--DGKDFCPLDF 419

Search completed: November 12, 2003, 14:33:21
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Computer Ltd.

ON protein - protein search, using sw mode:

Run on: November 12, 2003, 14:32:56 ; Search time 33 Seconds
(without alignments)
2310.809 Million cell updates/sec

Title: US-10-062-848-1
Perfect score: 2334
Sequence: 1 ASRQSCCTVDQGVQCFSE.....SFVRGLSFARSGGQWAECPA 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 3
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications Aa:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:
17: /cgn2_6/ptodata/1/pubpaa/US50_NEW_PUB.pep:
18: /cgn2_6/ptodata/1/pubpaa/US50_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	2334	100.0	444	15	US-10-062-848-1
2	2334	100.0	467	15	US-10-079-709-32
3	2334	100.0	467	15	US-10-229-358-5
4	2322	99.5	467	14	US-10-083-452-11
5	2302	98.6	462	15	US-10-229-358-12
6	2259	96.8	467	9	US-09-929-060-3
7	2255	96.6	443	9	US-09-929-060-1
8	2242	96.1	443	9	US-09-929-060-2
9	1971	84.4	410	15	US-10-229-358-11
10	1818	77.9	440	12	US-10-421-122-1
11	1818	77.9	467	14	US-10-083-452-9
12	1699	72.8	467	12	US-10-421-122-2
13	1606.5	68.8	449	15	US-10-062-848-12
14	1606.5	68.8	465	14	US-10-083-452-8
15	1606.5	68.8	465	15	US-10-062-848-78

16	1606.5	68.8	465	15	US-10-229-358-6
17	1606.5	68.8	474	15	US-10-213-930-24
18	1622.5	68.5	439	15	US-10-062-848-3
19	1598.5	68.5	465	15	US-10-062-848-80
20	1597.5	68.4	465	15	US-10-062-848-79
21	1594.5	68.3	465	15	US-10-062-848-81
22	1553.5	66.6	469	15	US-10-062-848-82
23	1532.5	65.7	447	15	US-10-062-848-6
24	1532.5	65.7	463	14	US-10-083-452-10
25	1520	65.1	450	15	US-10-062-848-15
26	1519	65.1	439	15	US-10-062-848-2
27	1513	64.8	489	15	US-10-229-358-4
28	1513	64.8	489	15	US-10-229-358-10
29	1496.5	64.1	450	15	US-10-062-848-9
30	1496.5	64.1	466	14	US-10-083-452-13
31	1493	64.0	466	14	US-10-083-452-12
32	1493	64.0	466	15	US-10-229-358-7
33	1222	52.4	475	14	US-10-083-452-14
34	1215	52.1	355	15	US-10-229-358-15
35	1156	49.5	478	14	US-10-083-452-3
36	1156	49.5	495	14	US-10-083-452-2
37	1129.5	48.4	487	14	US-10-083-452-15
38	1129.5	48.4	487	15	US-10-229-358-8
39	806	34.5	284	15	US-10-229-358-19
40	806	34.5	283	15	US-10-229-358-9
41	806	34.5	283	15	US-10-229-358-24
42	762.5	32.7	443	14	US-10-083-452-5
43	752.5	32.2	439	14	US-10-083-452-7
44	735.5	31.7	453	14	US-10-083-452-6
45	732	31.4	442	14	US-10-083-452-4

ALIGNMENTS

RESULT 1
US-10-062-848-1
; Sequence 1, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,948
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-062-848-1

Query Match	100.0%	Score 2334	DB 15	Length 444
Best Local Similarity	100.0%	Pred. No. 1.5e-224		
Matches 444	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Cy	1	ASRQSSCCTVDQGYQCFSESHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG	60	
Db	1	ASRQSSCCTVDQGYQCFSESHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG	60	
Cy	61	ARYPTDSKGGKKSALIEEIQONATTDDGKYAFUKTYNYSLGADDLTPFGQEQLVNSGIKF	120	
Db	61	ARYPTDSKGGKKSALIEEIQONATTDDGKYAFUKTYNYSLGADDLTPFGQEQLVNSGIKF	120	

```

QY 121 YRVESLIRNTPVPIRSGSRVTSAGKKTEEFQSTKLDPRAGQSGSPKIDVWISA 180
DB 121 YRVESLIRNTPVPIRSGSRVTSAGKKTEEFQSTKLDPRAGQSGSPKIDVWISA 180
QY 181 SSSNNTLDPGTCTVFESSEADTVANFTATFVPSIRORLENDLSGVTLTDEVTYLMOM 240
DB 181 SSSNNTLDPGTCTVFESSEADTVANFTATFVPSIRORLENDLSGVTLTDEVTYLMOM 240
QY 241 CSPTTISTSTVDTKLSFPCDLTHDEMINVDYLOSLLKYYGCHGAGNPLGTCGVGYANEL 300
DB 241 CSPTTISTSTVDTKLSFPCDLTHDEMINVDYLOSLLKYYGCHGAGNPLGTCGVGYANEL 300
QY 301 IARLTHSPVHDDTSSNNTLDSSPATFPLNSTLVADFSHENGIIISILFALGLVNGTKPLST 360
DB 301 IARLTHSPVHDDTSSNNTLDSSPATFPLNSTLVADFSHENGIIISILFALGLVNGTKPLST 360
QY 361 TTVENITQDGFSSAMTVPFASRLYVENMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
DB 361 TTVENITQDGFSSAMTVPFASRLYVENMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
DB 421 CTRDSFVRGLSFARSGGDWAECPA 444

```

RESULT 2

```

US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hattingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Juttin
; APPLICANT: Gerardus Seiten
; TITLE OF INVENTION: Cloning and Expression of Microbia.
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 32-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/668,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-26026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-079-709-32

```

```

Query Match 100.0%; Score 2334; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAVLSRHG 60
DB 24 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAVLSRHG 63
QY 61 ARVPTDSKGGKYSALIEEIQONATTEDGKYAFPLKTYNSLGGADLTFFGQEQLVNSGIKF 120
DB 84 ARVPTDSKGGKYSALIEEIQONATTEDGKYAFPLKTYNSLGGADLTFFGQEQLVNSGIKF 143
QY 121 YRVESLIRNTPVPIRSGSRVTSAGKKTEEFQSTKLDPRAGQSGSPKIDVWISA 180
DB 144 YRVESLIRNTPVPIRSGSRVTSAGKKTEEFQSTKLDPRAGQSGSPKIDVWISA 203
QY 181 SSSNNTLDPGTCTVFESSEADTVANFTATFVPSIRORLENDLSGVTLTDEVTYLMOM 240
DB 304 SSSNNTLDPGTCTVFESSEADTVANFTATFVPSIRORLENDLSGVTLTDEVTYLMOM 263
QY 241 CSPTTISTSTVDTKLSFPCDLTHDEMINVDYLOSLLKYYGCHGAGNPLGTCGVGYANEL 300
DB 264 CSPTTISTSTVDTKLSFPCDLTHDEMINVDYLOSLLKYYGCHGAGNPLGTCGVGYANEL 323
QY 301 IARLTHSPVHDDTSSNNTLDSSPATFPLNSTLVADFSHENGIIISILFALGLVNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNNTLDSSPATFPLNSTLVADFSHENGIIISILFALGLVNGTKPLST 383
QY 361 TTVENITQDGFSSAMTVPFASRLYVENMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 420
DB 384 TTVENITQDGFSSAMTVPFASRLYVENMOCQAEQEPVLRVLVNDRVVPLHGPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

```

RESULT 3

```

US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-229-358-5

```

```

Query Match 100.0%; Score 2334; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAVLSRHG 60
DB 24 ASRNQSCDVTVDQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFAVLSRHG 63
QY 61 ARVPTDSKGGKYSALIEEIQONATTEDGKYAFPLKTYNSLGGADLTFFGQEQLVNSGIKF 120

```



```

25 84 ARYPDSKGGKYSALIEEIQGNATTFDGKYAFKTKYNSLGGADLTPFGEDELVNSGKIF 143
QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 263
QY 241 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 300
DB 264 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 323
QY 301 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 360
DB 324 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 383
QY 361 TTVENITOTDGFSSAWTVPFASRLYVEMNQCAEQAEPLVRLVNDRVVPLHGCPCVDALGR 420
DB 384 TTVENITOTDGFSSAWTVPFASRLYVEMNQCAEQAEPLVRLVNDRVVPLHGCPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGQWAECEFA 444
DB 444 CTRDSFVRGLSFARSGGQWAECEFA 467

RESULT 4
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US2002012728A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.530-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/09/273,971
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 08407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 08806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 6C/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 6C/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficuum
US-10-083-452-11

Query Match 99.5%; Score 2322; DB 14; Length 467;
Best Local Similarity 99.5%; Pred. No. 2.5e-223;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVQGYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTTFAQVLSRHG 60
DB 24 ASRNOSSCDTVQGYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEEIQGNATTFDGKYAFKTKYNSLGGADLTPFGEDELVNSGKIF 120
DB 84 ARYPDSKGGKYSALIEEIQGNATTFDGKYAFKTKYNSLGGADLTPFGEDELVNSGKIF 143
QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 263
QY 241 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 300
DB 264 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 323
QY 301 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 360

```

```

DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 263
QY 241 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 300
DB 264 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 323
QY 301 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 360
DB 324 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 383
QY 361 TTVENITOTDGFSSAWTVPFASRLYVEMNQCAEQAEPLVRLVNDRVVPLHGCPCVDALGR 420
DB 384 TTVENITOTDGFSSAWTVPFASRLYVEMNQCAEQAEPLVRLVNDRVVPLHGCPCVDALGR 443
QY 421 CTRDSFVRGLSFARSGGQWAECEFA 444
DB 444 CTRDSFVRGLSFARSGGQWAECEFA 467

RESULT 5
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Tzinci, Anthony P.J.
; APPLICANT: Brookmar, Cayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 6C/48,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-12

Query Match 98.6%; Score 2302; DB 15; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.5e-221;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVQGYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTTFAQVLSRHG 60
DB 24 ASRNOSSCDTVQGYQCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEEIQGNATTFDGKYAFKTKYNSLGGADLTPFGEDELVNSGKIF 120
DB 84 ARYPDSKGGKYSALIEEIQGNATTFDGKYAFKTKYNSLGGADLTPFGEDELVNSGKIF 143
QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFEGFQSTKXKDPRAQPGQSSPKIDVWVISEA 203
QY 181 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVENAFATFVPSIRORLENDLSGVTLTDEVTYLMDM 263
QY 241 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 300
DB 264 CSFDTTISTVDTKLSPPFCDLFTHDEWINYDLSKKYKGAGNPLGPTQGVGYANEL 323
QY 301 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHNGIISLIFALGLYNGTKPLST 360

```



```
; APPLICANT: KONDO, HIDEASA
; APPLICANT: AWAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/329,063
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 0843:4/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)..(3)
; OTHER INFORMATION: Variable Amino Acid
; US-09-929-360-2

Query Match          96.1%; Score 2242; DB 9; Length 443;
Best Local Similarity 94.8%; Pred. No. 2.4e-215;
Matches 420; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 2 SRNCSCTVDCGYQCFSESHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHGA 61
DB 1 SXKQSTCDTVDCGYQCFSESHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHGA 60
QY 62 RYPTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 121
DB 61 RYPTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 120
QY 122 QRYESLTRNIVPFRSSGSSRVVIAAGKXFEIGFQSTKLKDPRAQFGQSSPKIDVWVISA 181
DB 121 QRYESLTRNIVPFRSSGSSRVVIAAGKXFEIGFQSTKLKDPRAQFGQSSPKIDVWVISA 180
QY 182 SSNNLTDPGCTCFVFESEADTVFANFTATFVPSIRQRLNDLSGVTLTDTETVYLMQW 241
DB 181 TSNNLTDPGCTCFVFESEADTVFANFTATFVPSIRQRLNDLSGVTLTDTETVYLMQW 240
QY 242 SPDTISTSTVDTKLSPPCDLFTHEEINVDYLSLKYKHGAGNPLGPTQGVYANELI 301
DB 241 SPDTISTSTVDTKLSPPCDLFTHEEINVDYLSLKYKHGAGNPLGPTQGVYANELI 300
QY 302 ARLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 361
DB 301 ARLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 360
QY 362 TVENITODGFSAMTVPPFASRLYVEMMQCQAEQEPVLRVYVNDRVVPLHGCPVDALGR 421
DB 361 TAENITODGFSAMTVPPFASRLYVEMMQCQAEQEPVLRVYVNDRVVPLHGCPVDALGR 420
QY 422 TRDSFVRGLSFARSGGDWAECPA 444
DB 421 TRDSFVRGLSFARSGGDWAECPA 443

RESULT 9
US-10-229-358-11
; Sequence 11, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
```

```
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-10-229-358-11

Query Match          84.4%; Score 1971; DB 15; Length 410;
Best Local Similarity 85.9%; Pred. No. 2.7e-188;
Matches 377; Conservative 8; Mismatches 2; Indels 52; Gaps 1;

QY 1 ASENQSSCDTVDCGYQCFSESHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHG 60
DB 24 ASRQSTCDTVDCGYQCFSESHLKGQYAPFFSLANESVISPEVAGCRVTFQAVLSRHG 59
QY 61 ARYFTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 120
DB 84 ARYFTDSKGGKYSALIEEIQONATTFDGKYAFVFLKTYNYSLGADLTPFGEQELVNSGKIF 143
QY 121 QRYESLTRNIVPFRSSGSSRVVIAAGKXFEIGFQSTKLKDPRAQFGQSSPKIDVWVISA 180
DB 144 QRYESLTRNIVPFRSSGSSRVVIAAGKXFEIGFQSTKLKDPRAQFGQSSPKIDVWVISA 203
QY 181 SSNNLTDPGCTCFVFESEADTVFANFTATFVPSIRQRLNDLSGVTLTDTETVYLMQW 240
DB 204 SSNNLTDPGCTCFVFESEADTVFANFTATFVPSIRQRLNDLSGVTLTDTETVYLMQW 212
QY 241 CSPDTISTSTVDTKLSPPCDLFTHEEINVDYLSLKYKHGAGNPLGPTQGVYANELI 300
DB 213 -SEDTISTSTVDTKLSPPCDLFTHEEINVDYLSLKYKHGAGNPLGPTQGVYANELI 271
QY 301 IASLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 360
DB 272 IASLTSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST 331
QY 361 TVENITODGFSAMTVPPFASRLYVEMMQCQAEQEPVLRVYVNDRVVPLHGCPVDALGR 420
DB 332 TVENITODGFSAMTVPPFASRLYVEMMQCQAEQEPVLRVYVNDRVVPLHGCPVDALGR 391
QY 421 CTDSFVRGLSFARSGGDW 439
DB 392 CTDSFVRGLSFARSGGDW 410

RESULT 10
US-10-421-112-1
; Sequence 1, Application US/10421112
; Publication No. US20030290677A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/10/421,112
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US/09/634,493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-10-421-112-1
```

```
Query Match          77.9%; Score 1818; DB 12; Length 441;
Best Local Similarity 76.6%; Pred. No. 64e-173;
Matches 338; Conservative 39; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 4 NOSCDTVDDGYOCFSETSHLWGOYAPFSSLANESVISPEVPAGCRVTFQAVLSRHGARY 63
DB 1 NSHSCDTVDDGYOCFPEISHLMGOYSPYFSEDESALSPDPDCRVTFVQVLSRHGARY 60
QY 64 PTDSKGGKYKYSALISEICQNAITFDGKYAFUKTYNYSLGADDLTFPGQOEUVNSGKIFYQR 123
DB 61 PISSKSKAYSALLLEAIOKNATAFKGYAFUKTYNITLGADDLTFPGENQVNSGKIFYRR 120
QY 124 YESLTRNIVPFIRSSGSRVIAASKKFIIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 193
DB 121 YKALARKIVPFIRASGSDRVIAAEKFIIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 190
QY 184 NNTLDPGTCVTFEDELADVEANFTATFVPS*RCQLEMLSGVLTLD*EVTVYMDMCSF 243
DB 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPQVTLTDEDVYVMDMCPF 240
QY 244 DTISTSTVDTKLSPFCDLFTHDEMIVNDY*QSLKKYVGHGAGNPLGPTQGVGVANELIAR 303
DB 241 ETVARTSDATELSPFCA*FTHDEWRQDY*QSLKKYVGHGAGNPLGPAQGVGFANELIAR 300
QY 304 LTHSPVHDDTSSNHTLDSSEATPPLNSTLYADFSHONGIISILFPA*GLYNGTKPLSTTV 363
DB 301 LTRSPVQDHTSTNHTLDSNPATPPLNATLYADESHONSMSISIFALGLYNGTAPLSTTV 360
QY 364 ENITQTQGFSSANTVPFASLYVEMMOCAEQSPLVRLVNDRVVPLHGCPVDALGRCTR 423
DB 361 ESIBETDGSASNTVPFGARAYVEMMOCAEKSPLVRLVNDRVVPLHGCAVCKLGRCKR 420
QY 424 DSFVRLGSFARSGGDWAECEFA 444
DB 421 DDFVEGLSFARSGGNWAECEFA 441
```

RESULT 11

```
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/99/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1995 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1996-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Variation
US-10-083-452-9
```

```
Query Match          77.9%; Score 1818; DB 14; Length 467;
Best Local Similarity 76.6%; Pred. No. 7e-173;
Matches 338; Conservative 39; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 4 NOSCDTVDDGYOCFSETSHLWGOYAPFSSLANESVISPEVPAGCRVTFQAVLSRHGARY 63
DB 27 NSHSCDTVDDGYOCFPEISHLMGOYSPYFSEDESALSPDPDCRVTFVQVLSRHGARY 86
QY 64 PTDSKGGKYKYSALISEICQNAITFDGKYAFUKTYNYSLGADDLTFPGQOEUVNSGKIFYQR 123
DB 87 PISSKSKAYSALLLEAIOKNATAFKGYAFUKTYNITLGADDLTFPGENQVNSGKIFYRR 146
QY 124 YESLTRNIVPFIRSSGSRVIAASKKFIIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 206
DB 147 YKALARKIVPFIRASGSDRVIAAEKFIIEGFSQAKLADPGSQPHQASPVLDVIFEGSGY 206
QY 184 NNTLDPGTCVTFEDELADVEANFTATFVPS*RCQLEMLSGVLTLD*EVTVYMDMCSF 243
DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPQVTLTDEDVYVMDMCPF 266
QY 244 DTISTSTVDTKLSPFCDLFTHDEMIVNDY*QSLKKYVGHGAGNPLGPTQGVGVANELIAR 303
DB 267 ETVARTSDATELSPFCA*FTHDEWRQDY*QSLKKYVGHGAGNPLGPAQGVGFANELIAR 326
QY 304 LTHSPVHDDTSSNHTLDSSEATPPLNSTLYADFSHONGIISILFPA*GLYNGTKPLSTTV 363
DB 327 LTRSPVQDHTSTNHTLDSNPATPPLNATLYADESHONSMSISIFALGLYNGTAPLSTTV 386
QY 364 ENITQTQGFSSANTVPFASLYVEMMOCAEQSPLVRLVNDRVVPLHGCPVDALGRCTR 423
DB 387 ESIBETDGSASNTVPFGARAYVEMMOCAEKSPLVRLVNDRVVPLHGCAVCKLGRCKR 446
QY 424 DSFVRLGSFARSGGDWAECEFA 444
DB 447 DDFVEGLSFARSGGNWAECEFA 467
```

RESULT 12

```
US-10-421-112-2
; Sequence 2, Application US/10421112
; Publication No. US20030190677A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/10/421,112
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US/99/634,493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-10-421-112-2
```

```
Query Match          72.8%; Score 1699; DB 12; Length 467;
Best Local Similarity 59.8%; Pred. No. 5.7e-16;
Matches 322; Conservative 38; Mismatches 61; Indels 40; Gaps 2;
```

QY 4 NOSCDTVDDGYOCFSETSHLWGOYAPFSSLANESVISPEVPAGCRVTFQAVLSRHGARY 63

```
DE 27 NSHSCDTVDGGYCCPEISHLWGQSPYFSELEDESAISPVDJCRVTFVQVLSRHGARY 86
QY 64 PTDEKGGKYKYSALIEIQONATTFDQKYAPJKTNYNSLGADDTJTFGEQELVNSGKIFYOR 123
DB 87 PTSSKSKAYS-----TNYNVLGACDCLTFPGENQMVNSGKIFYRR 126
QY 124 YESLTRNVFPIRSSGSSRVIASGKKFEGFCSTKLDPPRAOPGQSSPKID----- 174
DB 127 YKALARKVPIFRASGSDRVIAEAKFEGFCSTKLDPPRAOPGQSSPKID----- 196
QY 175 -----VWIEASSNNLTDPGTCTVFEDSELADTVEANFTATFVPSIRORLEND 223
DB 167 TAFKGYAFLXVILPEGSGYNNLTDHGCTAFEDSELCDVVEANFTALFAIRARLEAD 246
QY 224 LSGVTLTDEVTYLMXGSGFTISTISTVDTKLSFPCDLTFHDEMINVDYJSLKKYKYGHG 283
DB 247 LPGVTLTDEEDVYLMXGSGFTISTISTVDTKLSFPCDLTFHDEMINVDYJSLKKYKYG 306
QY 284 AGNPLGPTQGGYKAYNELIARLTHSPVHDTSSNHTLSSSPATFPNSTLYADFSHONGI 343
DB 307 AGNPLGPGAGGVGFANELIARLTHSPVHDTSSNHTLSSSPATFPNSTLYADFSHONGI 366
QY 344 SFFALGLYNGTKPLSTTTVENZTCTDGFSSAWTVPFASRLVEMQCCAEPLVRLVLY 403
DB 367 SFFALGLYNGTKPLSTTTVENZTCTDGFSSAWTVPFASRLVEMQCCAEPLVRLVLY 426
QY 404 NDRVPLHGCPVLCALGCTRTSFRVGLSFGSFGGDMWAECA 444
DB 427 NDRVPLHGCAVCKLGRCKRDFEGLSFGSFGGDMWAECA 467

RESULT 14
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TONSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WISS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12
```

```
Query Match 68.8%; Score 1606.5; DB 15; Length 449;
Best Local Similarity 66.4%; Pred. No. 9.6e-152;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
```

```
QY 1 ASRNSCSDTVDOGYOCFSETSHLWGQYAPFSLANESVISEVPAGCRVTFACVLSRHG 60
DB 7 SSAGSKSDTVDLGYQCSPATSHLWGQYSPFFSEJESVSSKJPKDCRITLVQVLSRHG 66
QY 61 ARYPTDSKGGKYSALIEIEIQONATTFDQKYAPJKTNYNSLGADDTJTFGEQELVNSGK 120
DB 67 ARYPTSSKGGKYSALIEIEIQONATTFDQKYAPJKTNYNSLGADDTJTFGEQELVNSGK 126
QY 121 YORYESLNRNIVPPIRSSGSSRVIASGKKFIEGFCSTKLDPPRAOPGQSSPKIDVISEA 160
DB 127 YORYKALARSVVVPIFRASGSDRVIAEAKFEGFCSTKLDPPRAOPGQSSPKIDVISEA 185
```

```
QY 181 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDJSGVTLTDEVTYLMXDM 240
DB 186 ETPFNNTLDHGVCTKFEASQLGDEVAANFTALFAIRARAEKHLPGVTLTDEEDVYLSMDM 245
QY 241 CSFDDTSTSTVDTKLSFPCDLTFHDEMINVDYJSLKKYKYGAGNPLGPTQGGYKAYNEL 300
DB 246 CSFDTVARTSDASQUSFFCQFTHNEWKYNYLQSLGKYYGYAGNPLGPTQGGYKAYNEL 305
QY 301 IARLTHSPVHDTSSNHTLSSSPATFPNSTLYADFSHONGIISLFLALGLYNGTKPLST 360
DB 306 IARLTHSPVHDTSSNHTLSSSPATFPNSTLYADFSHONGIISLFLALGLYNGTKPLST 365
QY 361 TTVENITQDGFSSAWTVPFASRLVEMQCCAEPLVRLVLYADFSHONGIISLFLALGLY 420
DB 366 TTVENITQDGFSSAWTVPFASRLVEMQCCAEPLVRLVLYADFSHONGIISLFLALGLY 425
QY 421 CTRDSFVRSLSEAFSGGDMWAECA 444
DB 426 CTRDSFVRSLSEAFSGGDMWAECA 449

RESULT 14
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,671
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/050,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8
```

```
Query Match 68.8%; Score 1606.5; DB 14; Length 465;
Best Local Similarity 66.4%; Pred. No. 1e-151;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
```

```
QY 1 ASRNSCSDTVDOGYOCFSETSHLWGQYAPFSLANESVISEVPAGCRVTFACVLSRHG 60
DB 23 SSAGSKSDTVDLGYQCSPATSHLWGQYSPFFSEJESVSSKJPKDCRITLVQVLSRHG 82
QY 61 ARYPTDSKGGKYSALIEIEIQONATTFDQKYAPJKTNYNSLGADDTJTFGEQELVNSGK 120
DB 83 ARYPTSSKGGKYSALIEIEIQONATTFDQKYAPJKTNYNSLGADDTJTFGEQELVNSGK 142
QY 121 YORYESLNRNIVPPIRSSGSSRVIASGKKFIEGFCSTKLDPPRAOPGQSSPKIDVISEA 180
DB 143 YORYKALARSVVVPIFRASGSDRVIAEAKFIEGFCSTKLDPPRAOPGQSSPKIDVISEA 201
QY 181 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDJSGVTLTDEVTYLMXDM 240
DB 202 ETPFNNTLDHGVCTKFEASQLGDEVAANFTALFAIRARAEKHLPGVTLTDEEDVYLSMDM 261
```

QY 241 CSFDTISTSTVDTKLSPFCDLFTDHEWNYDYQLSKKXYGKAGNP-GPTQGYGANEL 300
 DB 242 CSFDTVARTSDASQSPFCCLFTNHEWKNYVQLSKKXYGKAGNP-GPAQGGFTNEL 321
 QY 301 IARLTHSPVHDTSSNHTLDCSPATFPPLNSTLYADFSDHNGIIS-LFALGLYNGTKPLST 360
 DB 322 IARLTRSPVQCHTSTNSTLVSNPATFPPLNATYVDFSHDNKXVSIFFFALGLYNGTEPLSR 381
 QY 361 TTVENITQTDGSSANTVPFASRLYVEMMOCAEQEPLVRV-VNDRVVPJHGCPCVALGR 420
 DB 382 TSVESAKELDGYASASWVPFGARAYFETMOCKSEKEPLVRALINDRVVPLHGCCDVKJGR 441
 QY 421 CTRDSFVRGLSPARSGGDWAECPA 444
 DB 442 CKLNDFFVKGLSWARSGGNWGECPA 465

RESULT 15
 US-10-062-848-78
 ; Sequence 78, Application US/10662848
 ; Publication No. US2003032155A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTREWA, Dirk
 ; APPLICANT: PASAMONTES, Luis
 ; APPLICANT: TOMSCHY, Andrea
 ; APPLICANT: van LOON, Adolphus
 ; APPLICANT: VOGEL, Kurt
 ; APPLICANT: WYSS, Markus
 ; TITLE OF INVENTION: MODIFIED PHYTASES
 ; FILE REFERENCE: Modified Phytases
 ; CURRENT APPLICATION NUMBER: US/10/062,848
 ; CURRENT FILING DATE: 2002-02-01
 ; PRIOR APPLICATION NUMBER: 09/044,718
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: EP 97810175.6
 ; PRIOR FILING DATE: 1997-03-25
 ; NUMBER OF SEQ ID NOS: 82
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 78
 ; TYPE: PRI
 ; ORGANISM: Aspergillus fumigatus
 US-10-062-848-78

Query Match 68.8%; Score 1606.5; DB 15; Length 465;
 Best Local Similarity 66.4%; Pred. No. 1e-151;
 Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 1 ASRNOSSCDTVQGYQCFSETSHLWGQYAPFFPSLANESVISPEVPAGCRVTFACVLSRHG 60
 DB 23 SSAGSKSCD*VDLGYQCSPATSHLWGQYSPFFPS*EDELVSSSKLPKDCR*TLVQVLSRHG 82
 QY 61 ARYPTDSKKNYSALJEEICQNAITFDGKYAFUKTYNS:GADDJTPFGECJHNSG:KF 120
 DB 83 ARYPTSKSKKYYKCLVTAICANATDFKGFAPLXTNYT:GADDCJTPFGECQLWNSG:KF 142
 QY 121 YORYESJTRNIVPFISSGSSRVIASGKKFIEGFSQTKLKDFPRAQFGSSPKIDVVISIA 130
 DB 143 YORYKALARSVPFIRASGSDRVIASGEKIEGFOQAKLADPGA-TNRAAPALSVIIPS 201
 QY 181 SSNNITLDPGCTCTFESELSADTVEANFTATVPFSIRQRLNLSGVLTDTFTVYLYXDM 240
 DB 202 ETFTNTLDHGVTCKFEASQLGDEVAANFTALFAPDIRAPAEKELPGVTJTDSDVSLXDM 261
 QY 241 CSFDTISTSTVDTKLSPFCDLFTDHEWNYDYQLSKKXYGKAGNP-GPTQGYGANEL 300
 DB 262 CSFDTVARTSDASQSPFCCLFTNHEWKNYVQLSKKXYGKAGNP-GPAQGGFTNEL 321
 QY 301 IARLTHSPVHDTSSNHTLDCSPATFPPLNSTLYADFSDHNGIIS-LFALGLYNGTKPLST 360
 DB 322 IARLTRSPVQCHTSTNSTLVSNPATFPPLNATYVDFSHDNKXVSIFFFALGLYNGTEPLSR 381

QY 361 TTVENITQTDGSSANTVPFASRLYVEMMOCAEQEPLVRV-VNDRVVPJHGCPCVALGR 420
 DB 382 TSVESAKELDGYASASWVPFGARAYFETMOCKSEKEPLVRALINDRVVPLHGCCDVKJGR 441
 QY 421 CTRDSFVRGLSPARSGGDWAECPA 444
 DB 442 CKLNDFFVKGLSWARSGGNWGECPA 465

Search completed: November 12, 2003, 14:38:19
 Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 14:30:30 ; Search time 21 Seconds
(without alignments)
894.572 Million cell updates/sec

Title: US-10-062-848-1
Perfect score: 2334
Sequence: 1 ASRNQSSCDTVQGYQCFSE.....SFVRGLSFARSGDWAECFA 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A_COXB pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COXB pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COXB pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COXB pep.*
5: /cgn2_6/ptodata/1/iaa/FCFUS_COXB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	444	4	US-09-044-718-1 Sequence 1, Appl.
2	2334	100.0	467	1	US-08-151-574-32 Sequence 32, App.
3	2334	100.0	467	1	US-08-146-424-20 Sequence 20, App.
4	2334	100.0	467	1	US-08-603-759-2 Sequence 2, Appl.
5	2334	100.0	467	2	US-08-419-448-32 Sequence 32, App.
6	2334	100.0	467	2	US-08-819-825-3 Sequence 3, Appl.
7	2334	100.0	467	3	US-09-163-642-3 Sequence 3, Appl.
8	2334	100.0	467	4	US-09-233-510-32 Sequence 32, Appl.
9	2334	100.0	467	4	US-09-636-499-5 Sequence 5, Appl.
10	2322	99.5	467	4	US-09-273-871A-11 Sequence 11, App.
11	2302	98.6	462	4	US-09-636-499-12 Sequence 12, App.
12	2290	98.1	467	2	US-07-923-724-8 Sequence 8, Appl.
13	2290	98.1	467	2	US-08-609-426A-8 Sequence 8, Appl.
14	2290	98.1	467	3	US-08-374-652C-2 Sequence 2, Appl.
15	2259	96.8	467	3	US-09-155-855-3 Sequence 3, Appl.
16	2259	96.8	467	4	US-09-543-744-3 Sequence 3, Appl.
17	2259	96.8	467	4	US-09-929-060-3 Sequence 3, Appl.
18	2255	96.6	443	3	US-09-155-855-1 Sequence 1, Appl.
19	2255	96.6	443	4	US-09-543-744-1 Sequence 1, Appl.
20	2255	96.6	443	4	US-09-929-060-1 Sequence 1, Appl.
21	2242	96.1	443	3	US-09-155-855-2 Sequence 2, Appl.
22	2242	96.1	443	4	US-09-543-744-2 Sequence 2, Appl.
23	2242	96.1	443	4	US-09-929-060-2 Sequence 2, Appl.
24	1971	84.4	410	4	US-09-636-499-11 Sequence 11, Appl.
25	1818	77.9	441	3	US-09-221-425-1 Sequence 1, Appl.
26	1818	77.9	441	4	US-09-634-493A-1 Sequence 1, Appl.
27	1818	77.9	467	4	US-09-273-871A-9 Sequence 9, Appl.

28	1751	75.0	466	3	US-08-869-435-12 Sequence 12, Appl.
29	1751	75.0	466	4	US-08-744-231-12 Sequence 12, App.
30	1693	72.8	467	3	US-09-121-425-2 Sequence 2, Appl.
31	1693	72.8	467	4	US-09-634-403A-2 Sequence 2, Appl.
32	1606.5	69.8	449	4	US-09-044-718-12 Sequence 12, Appl.
33	1606.5	69.8	465	3	US-08-869-435-33 Sequence 33, Appl.
34	1606.5	69.8	465	4	US-08-744-231-33 Sequence 33, Appl.
35	1606.5	69.8	465	4	US-09-044-718-78 Sequence 78, Appl.
36	1606.5	69.8	465	4	US-09-636-499-6 Sequence 6, Appl.
37	1606.5	69.8	465	4	US-09-273-871A-2 Sequence 8, Appl.
38	1602.5	68.7	439	4	US-09-044-718-3 Sequence 3, Appl.
39	1598.5	68.5	465	4	US-09-044-718-80 Sequence 80, Appl.
40	1597.5	68.4	465	4	US-09-044-718-79 Sequence 79, Appl.
41	1594.5	68.3	465	4	US-09-044-718-81 Sequence 81, Appl.
42	1553.5	66.6	469	4	US-09-044-718-82 Sequence 82, Appl.
43	1532.5	65.7	447	4	US-09-044-718-6 Sequence 6, Appl.
44	1532.5	65.7	463	3	US-08-868-435-29 Sequence 29, Appl.
45	1532.5	65.7	463	4	US-08-744-231-29 Sequence 29, Appl.

ALIGNMENTS

RESULT 1
US-09-044-718-1
Sequence 1, Application US/0904471-8
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: VAN LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WISS, Markus
TITLE OF INVENTION: MODIFIED PHYLASES
FILE REFERENCE: Modified Phylases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRICER APPLICATION NUMBER: EP 978,0175.6
PRICER FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 444
TYPE: PPT
ORGANISM: Aspergillus niger
US-09-044-718-1
Query Match : 100.0%; Score 2334; DB 4; Length 444;
Best local Similarity : 100.0%; Pred. No. 1.1e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASRNQSSCDTVQGYQCFSESHLWQVAPFFSLANESVISPEVPAGCRVTFAQVLSRHG 60	
DB	1	ASRNQSSCDTVQGYQCFSESHLWQVAPFFSLANESVISPEVPAGCRVTFAQVLSRHG 60	
QY	61	ARYPTDSKGGKYSALIEE:QQNATFDGKYALKKNYSLGADLTTPGEQLVNSGIKF 120	
DB	61	ARYPTDSKGGKYSALIEE:QQNATFDGKYALKKNYSLGADLTTPGEQLVNSGIKF 120	
QY	121	YORYESLTNIVPFRSSGSSRVIASGKXKFIQGFSTKLDPRAOPGQSSPKIDVVISIA 180	
DB	121	YORYESLTNIVPFRSSGSSRVIASGKXKFIQGFSTKLDPRAOPGQSSPKIDVVISIA 180	
QY	181	SSNNLTDPGCTCTVEFDSSELADTVEANFTATVPISIRQLENDLSGVLTJDTDEVYLMOM 240	
DB	181	SSNNLTDPGCTCTVEFDSSELADTVEANFTATVPISIRQLENDLSGVLTJDTDEVYLMOM 240	
QY	241	CSFDITSTSTVDTK:SPFCDLTHDEWINDYLOSLKKYKYGAGNPLGPTGCVANEL 300	
DB	241	CSFDITSTSTVDTK:SPFCDLTHDEWINDYLOSLKKYKYGAGNPLGPTGCVANEL 300	
QY	301	IARLTHSPVHDDTSSNHTLDSSTPATFPLNSTLYADFSDHNGIISILFALGLYNG-KPLST 360	

DB 301 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGYNKTKPST 360
QY 361 TTVENITOTDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGGCPVDALGR 420
DB 361 TTVENITOTDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGGCPVDALGR 420
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
DB 421 CTRDSFVRGLSFARSGGDWAECEFA 444

RESULT 2
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. van Paridon
; APPLICANT: Annemarie E. Veerstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Setten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/698,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-151-574-32

Query Match 100.0%; Score 2334; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNSQSCDVTVDGQYQCFSETSLWQCYAPFFSLANESVISEVPAGRCVTPAQVLSRHG 60
DB 24 ASRNSQSCDVTVDGQYQCFSETSLWQCYAPFFSLANESVISEVPAGRCVTPAQVLSRHG 83
QY 61 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADDTTPFGEQELVNSGKIF 120
DB 84 ARYPTDSKGGKYSALIEECQNATTFDGKYAFUKTYNYSLGADDTTPFGEQELVNSGKIF 143
QY 121 YQYVESLTRNIVPFISSGSSSRVIASGKRFIEGFQSKLKDPRAQPGQSSPKIDVWVISEA 180

DB 144 YQYVESLTRNIVPFISSGSSSRVIASGKRFIEGFQSKLKDPRAQPGQSSPKIDVWVISEA 203
QY 181 SSNNNTLDGTCITVFEDSELADTVEANFTATFVPS:RORLENDLSGVTLTDTDEVLYLMDX 240
DB 204 SSNNNTLDGTCITVFEDSELADTVEANFTATFVPS:RORLENDLSGVTLTDTDEVLYLMDX 263
QY 241 CSFDTTSTSTVTKLSPPCDLFTHDENINYDYLCSLKKYKHGAGNPLGPTOGVYANEL 300
DB 264 CSFDTTSTSTVTKLSPPCDLFTHDENINYDYLCSLKKYKHGAGNPLGPTOGVYANEL 323
QY 301 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGYNKTKPST 360
DB 324 IARLTHSPVHDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISLFAALGYNKTKPST 383
QY 361 TTVENITOTDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGGCPVDALGR 420
DB 394 TTVENITOTDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGGCPVDALGR 443
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
DB 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 3
US-08-146-424-20
; Sequence 20, Application US/08-46424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRAJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: S-JMONS, PETER C.
; APPLICANT: VERMOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-146-424-20

Query Match 100.0%; Score 2334; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CY 1 ASRNSCCTVDGQYCCFSETSHLMGOYAPFSLANESVISPEVPAGCRVTFACVLSRRG 60
DB 24 ASRNSCCTVDGQYCCFSETSHLMGOYAPFSLANESVISPEVPAGCRVTFACVLSRRG 83
CY 61 ARYPDSKGGKYSALIEEIQONATTFDGYAFKTYNSLGADDLTPFGQELVNSGKIF 120
DB 84 ARYPDSKGGKYSALIEEIQONATTFDGYAFKTYNSLGADDLTPFGQELVNSGKIF 143
CY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKOPRAQPGQSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKOPRAQPGQSSPKIDVWVISEA 203
CY 181 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPISRQRLNCLSGVTLTDEVTYLMGX 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPISRQRLNCLSGVTLTDEVTYLMGX 263
CY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 323
CY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNG--ISILPALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNG--ISILPALGLYNGTKPLST 383
CY 361 TTVENITQTDGFSASNTVPFASRLYVEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 420
DB 384 TTVENITQTDGFSASNTVPFASRLYVEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 443
CY 421 CTRDSFVRGLSPARSGGWAECFA 444
DB 444 CTRDSFVRGLSPARSGGWAECFA 467

RESULT 4
US-08-693-709-2
: Sequence 2, Application: US/08693709
: Patent No. 5770413
: GENERAL INFORMATION:
: APPLICANT: VAN OOIJEN, ALBERT J.J.
: APPLICANT: RIETVELD, KRIJN
: APPLICANT: HOEKEMA, ANDREAS
: APPLICANT: PEN, JAN
: APPLICANT: SJOEMERS, PETER C.
: APPLICANT: VERWOED, TEUNIS C.
: TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
: TITLE OF INVENTION: IN PLANTS
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693,709
: FILING DATE: 07-AUG-1996
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/146,424
: FILING DATE: 02-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24615-20011.10
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-813-5600
: TELEFAX: 415-494-0792

```

```

TELEX: 706141
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal
: FEATURE:
: NAME/KEY: Signal Sequence
: LOCATION: 1..23
: OTHER INFORMATION:
: US-08-693-709-2

Query Match: 100.0% Score 2334; DB 1: Length 467;
Best Local Similarity 100.0% Pred. No. 1.2e-2332;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ASRNSCCTVDGQYCCFSETSHLMGOYAPFSLANESVISPEVPAGCRVTFACVLSRRG 60
DB 24 ASRNSCCTVDGQYCCFSETSHLMGOYAPFSLANESVISPEVPAGCRVTFACVLSRRG 83
CY 61 ARYPDSKGGKYSALIEEIQONATTFDGYAFKTYNSLGADDLTPFGQELVNSGKIF 120
DB 84 ARYPDSKGGKYSALIEEIQONATTFDGYAFKTYNSLGADDLTPFGQELVNSGKIF 143
CY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKOPRAQPGQSSPKIDVWVISEA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKOPRAQPGQSSPKIDVWVISEA 203
CY 181 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPISRQRLNCLSGVTLTDEVTYLMGX 240
DB 204 SSSNNTLDPGCTCTVFEDSELADTVANFTATVPISRQRLNCLSGVTLTDEVTYLMGX 263
CY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSLKKYVGHGAGNPLGPTCGVGYANEL 323
CY 301 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNG--ISILPALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNG--ISILPALGLYNGTKPLST 383
CY 361 TTVENITQTDGFSASNTVPFASRLYVEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 420
DB 384 TTVENITQTDGFSASNTVPFASRLYVEMMCCQAECEPLRVLVNDRVVPJHGCPCVDAJGR 443
CY 421 CTRDSFVRGLSPARSGGWAECFA 444
DB 444 CTRDSFVRGLSPARSGGWAECFA 467

RESULT 5
US-08-419-448-32
: Sequence 32, Application: US/08419448
: Patent No. 5863533
: GENERAL INFORMATION:
: APPLICANT: Robert F.X. Van Gorkom
: APPLICANT: Willem Van Hartingsveldt
: APPLICANT: Petrus A. Van Paridon
: APPLICANT: Annemarie E. Veenstra
: APPLICANT: Rudolf G.M. Luttir
: APPLICANT: Gerardus Selten
: TITLE OF INVENTION: Cloning and Expression of Microbial
: TITLE OF INVENTION: Phytase
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20006-1888

```

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,448
 FILING DATE: 10-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-597-1500
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-419-448-32

Query Match 100.0%; Score 2334; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2e-232;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASRNOSSCDTVDCGYQCFSESHLWGYAPFFSLANESVISPVPAGCRVTPAQLVSRHG	60
DB	24	ASRNOSSCDTVDCGYQCFSESHLWGYAPFFSLANESVISPVPAGCRVTPAQLVSRHG	93
QY	61	ARYPTDSKGYKYSALIEIQONATTFGKYAFILKTYNSLGGADLTPFGQEQLVNSGKIF	120
DB	84	ARYPTDSKGYKYSALIEIQONATTFGKYAFILKTYNSLGGADLTPFGQEQLVNSGKIF	143
QY	121	YQRYESLTRNIVPIRSGSSRVIASGKPIEGFQSTKLKDPRAQCGSSPKIDVWVSEA	180
DB	144	YQRYESLTRNIVPIRSGSSRVIASGKPIEGFQSTKLKDPRAQCGSSPKIDVWVSEA	203
QY	181	SSSNTLDPGCTCTVFDESELADTVEANFTATFVPSIRORLENDLSGVTLDTEVTYLMEM	240
DB	204	SSSNTLDPGCTCTVFDESELADTVEANFTATFVPSIRORLENDLSGVTLDTEVTYLMEM	263
QY	241	CSFTTISTSTVDTKLSPPFCOLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANEL	300
DB	264	CSFTTISTSTVDTKLSPPFCOLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANEL	323
QY	301	IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST	360
DB	324	IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST	383
QY	361	TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPPLVRLVNDRVVPLHGGCPVDALGR	420
DB	384	TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPPLVRLVNDRVVPLHGGCPVDALGR	443
QY	421	CTRDSFVRGLSFARSGGDWAECEFA	444
DB	444	CTRDSFVRGLSFARSGGDWAECEFA	467

RESULT 6
 US-08-419-825-3
 ; Sequence 3, Application US/088:9625
 ; Patent No. 5866118
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Ray, Michael W.
 ; APPLICANT: Klosz, Alan V.
 ; TITLE OF INVENTION: Polypeptides Having Phytase Activity
 ; TITLE OF INVENTION: And Nucleic Acids Encoding Same
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:

ADDRESSSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/619,825
 FILING DATE: 18-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias C.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4758.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 5123
 TELEFAX: 212 867 0258
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-619-825-3

Query Match 100.0%; Score 2334; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2e-232;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASRNOSSCDTVDCGYQCFSESHLWGYAPFFSLANESVISPVPAGCRVTPAQLVSRHG	60
DB	24	ASRNOSSCDTVDCGYQCFSESHLWGYAPFFSLANESVISPVPAGCRVTPAQLVSRHG	83
QY	61	ARYPTDSKGYKYSALIEIQONATTFGKYAFILKTYNSLGGADLTPFGQEQLVNSGKIF	120
DB	84	ARYPTDSKGYKYSALIEIQONATTFGKYAFILKTYNSLGGADLTPFGQEQLVNSGKIF	143
QY	121	YQRYESLTRNIVPIRSGSSRVIASGKPIEGFQSTKLKDPRAQCGSSPKIDVWVSEA	180
DB	144	YQRYESLTRNIVPIRSGSSRVIASGKPIEGFQSTKLKDPRAQCGSSPKIDVWVSEA	203
QY	181	SSSNTLDPGCTCTVFDESELADTVEANFTATFVPSIRORLENDLSGVTLDTEVTYLMEM	240
DB	204	SSSNTLDPGCTCTVFDESELADTVEANFTATFVPSIRORLENDLSGVTLDTEVTYLMEM	263
QY	241	CSFTTISTSTVDTKLSPPFCOLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANEL	300
DB	264	CSFTTISTSTVDTKLSPPFCOLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANEL	323
QY	301	IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST	360
DB	324	IARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHONGIISILFALGLYNGTKPLST	383
QY	361	TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPPLVRLVNDRVVPLHGGCPVDALGR	420
DB	384	TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPPLVRLVNDRVVPLHGGCPVDALGR	443
QY	421	CTRDSFVRGLSFARSGGDWAECEFA	444
DB	444	CTRDSFVRGLSFARSGGDWAECEFA	467

RESULT 7
 US-09-163-642-3
 ; Sequence 3, Application US/09:63642
 ; Patent No. 6221644
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.

APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
STREET: 405 Lexington Avenue, Suite 640C
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Iambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 3298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-163-642-3

Query Match 100.0%; Score 2334; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 60
|||||
DB 24 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 83
|||||

QY 61 ARYPTDSKGGKYSAL--EEIQONATTFDQKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 120
|||||
DB 84 ARYPTDSKGGKYSAL--EEIQONATTFDQKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 143
|||||

QY 121 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQSSPKIDVWVSEA 180
|||||
DB 144 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQSSPKIDVWVSEA 203
|||||

QY 181 SSSNNLTDPGCTVPDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDM 240
|||||
DB 204 SSSNNLTDPGCTVPDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDM 263
|||||

QY 241 CSFDTISTSTVDTKLSPFCDLFTDQWYNYDQSLKKYHGHGAGNPLGTQGVGYANEL 300
|||||
DB 264 CSFDTISTSTVDTKLSPFCDLFTDQWYNYDQSLKKYHGHGAGNPLGTQGVGYANEL 323
|||||

QY 301 IARLTHSPVHDDTSNNHLLDSSPATFPNSTYADPFSHDNGIIISILFALGLYNGTKPLST 360
|||||
DB 324 IARLTHSPVHDDTSNNHLLDSSPATFPNSTYADPFSHDNGIIISILFALGLYNGTKPLST 383
|||||

QY 361 TTVENITQDGFSSAWTVFASRLVEMMQOAEQELVLRVNDVRVPLHSCVPDALGR 420
|||||
DB 384 TTVENITQDGFSSAWTVFASRLVEMMQOAEQELVLRVNDVRVPLHSCVPDALGR 443
|||||

QY 421 CTRDSFVRGLSPARSGGDWAECEFA 444
|||||

DB 444 CTRDSFVRGLSPARSGGDWAECEFA 467

RESULT 8
US-09-233-510-32
Sequence 32, Application US/092335-0
Patent No. 6350602
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seinen
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 57/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-233-510-32

Query Match 100.0%; Score 2334; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 60
|||||
DB 24 ASRNQSSCTVDQGYOCFSETSHLWQYAPFFSLANESVISPVEPAGCRVTFQAQLSRHG 83
|||||

QY 61 ARYPTDSKGGKYSALIEETQONATTFDQKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 120
|||||
DB 84 ARYPTDSKGGKYSALIEETQONATTFDQKYAFKTYNYSLGADDLTPFGEQELVNSGKIF 143
|||||

QY 121 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQSSPKIDVWVSEA 180
|||||
DB 144 YORYESLNRNIVPFRSSGSSRVIASGKKFIEGFQSTKPKDPRACQSSPKIDVWVSEA 203
|||||

QY 181 SSSNNLTDPGCTVPDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDM 240
|||||
DB 204 SSSNNLTDPGCTVPDESELADTVEANFTATFVPSIRORLENDLSGVTLTDTETVYLMDM 263
|||||

QY 241 CSFDTISTSTVDTKLSPFCDLFTDQWYNYDQSLKKYHGHGAGNPLGTQGVGYANEL 300
|||||

```

Db 264 CSFDTISTVTQKLSPPCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
Qy 301 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
Qy 361 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
Qy 421 CTRDSFVRGLSFARSGGDWAECPA 444
Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 9
US-09-636-499-5
; Sequence 5, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-636-499-5

Query Match 100.0%; Score 2334; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 60
Db 24 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 83
Qy 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNSLSGADDLTPFGQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNSLSGADDLTPFGQELVNSGKIF 143
Qy 121 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVVISIA 180
Db 144 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVVISIA 203
Qy 181 SSSNNTLDPGTCTVFEDESLADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 240
Db 204 SSSNNTLDPGTCTVFEDESLADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 263
Qy 241 CSFDTISTVTQKLSPPCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 300
Db 264 CSFDTISTVTQKLSPPCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
Qy 301 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
Qy 361 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
Qy 421 CTRDSFVRGLSFARSGGDWAECPA 444

```

```

Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 10
US-09-273-871A-11
; Sequence 11, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.50C-JS
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficuum
US-09-273-871A-11

Query Match 99.5%; Score 2322; DB 4; Length 467;
Best Local Similarity 99.5%; Pred. No. 2.1e-231;
Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 60
Db 24 ASRNQSSCDTVQGYOCFSETSHLWQYAPFFSLANESVISPEVPAGCRVTPAQVLSRHG 83
Qy 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNSLSGADDLTPFGQELVNSGKIF 120
Db 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNSLSGADDLTPFGQELVNSGKIF 143
Qy 121 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVVISIA 180
Db 144 YQYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAGQSSPKIDVVISIA 203
Qy 181 SSSNNTLDPGTCTVFEDESLADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 240
Db 204 SSSNNTLDPGTCTVFEDESLADTVEANFTATVPFSIRQLENDLSGVTLTDEVTYMDM 263
Qy 241 CSFDTISTVTQKLSPPCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 300
Db 264 CSFDTISTVTQKLSPPCDLTHDEWYNDYLSKYYGSGAGNPLGPTQGVYANEL 323
Qy 301 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Db 324 IARLTHSPVHDDTSSNHTLDSSPATPPNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
Qy 361 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 420
Db 384 TTVENITQTDGSSAWTPFASRLYVENMCCOAEQPLVRVLVNDRVVPLHGCPCVDALGR 443
Qy 421 CTRDSFVRGLSFARSGGDWAECPA 444
Db 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 11
US-09-636-499-12
; Sequence 12, Application US/09636499

```

```

Patent No. 6475762
GENERAL INFORMATION:
APPLICANT: Stafford, Christian F.
APPLICANT: Trinci, Anthony P.J.
APPLICANT: Brookman, Jayne L.
TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
FILE REFERENCE: G586-2
CURRENT APPLICATION NUMBER: US/99/636,499
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,963
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 462
TYPE: PRT
ORGANISM: Aspergillus niger
US-09-636-499-12

Query Match 98.6% Score 2302; DB 4; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.4e-229;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDQGYCCFSESHLWGQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNOSSCDTVDQGYCCFSESHLWGQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSLGADDLTPFGEGLVNSGIKF 120
DB 84 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSLGADDLTPFGEGLVNSGIKF 143
QY 121 YORYESLIRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWVISEA 180
DB 144 YORYESLIRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTVFEDELADTVENATFATFASIRORLENDLSGVLTDTTEVTYMDM 240
DB 204 SSSNNTLDPGCTVFEDELADTVENATFATFASIRORLENDLSGVLTDTTEVTYMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYLOSJKKYYGHGAGNFIPTQGGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYLOSJKKYYGHGAGNFIPTQGGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 383
QY 361 TVVENITQDGFSSAWTVFASRLVYEMNQCAQCEPLRVLVNDRVVPVPHGCPVDALGR 420
DB 384 TVVENITQDGFSSAWTVFASRLVYEMNQCAQCEPLRVLVNDRVVPVPHGCPVDALGR 443

RESULT 12
US-C7-923-724-8
Sequence 8, Application US/C7923724
Patent No. 5780292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Maria T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Fiddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Maria K.
APPLICANT: Fagerström, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma

```

```

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-724-8

Query Match 98.1% Score 2290; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 4.2e-228;
Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNOSSCDTVDQGYCCFSESHLWGQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 60
DB 24 ASRNOSSCDTVDQGYCCFSESHLWGQYAPFSLANESVISPEVPAGCRVTFAQVLSRHG 83
QY 61 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSLGADDLTPFGEGLVNSGIKF 120
DB 84 ARYPDSKGGKYSALIEIQNATTFDQKYAFLKTYNYSLGADDLTPFGEGLVNSGIKF 143
QY 121 YORYESLIRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWVISEA 180
DB 144 YORYESLIRNIVPFIIRSSGSRVZASGKKFIEGPOSTKLKDPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTVFEDELADTVENATFATFASIRORLENDLSGVLTDTTEVTYMDM 240
DB 204 SSSNNTLDPGCTVFEDELADTVENATFATFASIRORLENDLSGVLTDTTEVTYMDM 263
QY 241 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYLOSJKKYYGHGAGNFIPTQGGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPFCDLFTHDEWINDYLOSJKKYYGHGAGNFIPTQGGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 383
QY 361 TVVENITQDGFSSAWTVFASRLVYEMNQCAQCEPLRVLVNDRVVPVPHGCPVDALGR 420
DB 384 TVVENITQDGFSSAWTVFASRLVYEMNQCAQCEPLRVLVNDRVVPVPHGCPVDALGR 443

```

```

QY 421 CTRDSFVRG-SFARSGGDWAECSA 444
DB 444 CTRDSFVRG-SFARSGGDWAECSA 467

RESULT 13
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 583733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstrom, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1103 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/046,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant B.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-426A-8

Query Match 98.1%; Score 2290; DB 2: Length 457;
Best Local Similarity 97.3%; Pred. No. 4,2e-226;
Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNSGCVDDGOCFSTSLWQYAPFFSLANESVTSFVPAGCAVTTAQLVSRHG 60
DB 24 ASRNSGCVDDGOCFSTSLWQYAPFFSLANESVTSFVPAGCAVTTAQLVSRHG 83

QY 61 ARYPTSGKKYKYSALIEEIQONATTFDGYAFKTYNYSJGADLTTPGQELVNSGKIF 120
DB 84 ARYPTSGKKYKYSALIEEIQONATTFDGYAFKTYNYSJGADLTTPGQELVNSGKIF 143
QY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGPOSTKLKOPRAGPGSSPKIDVVVISEA 180
DB 144 YORYESLTRNIVPFISSGSSRVIASGKKFIEGPOSTKLKOPRAGPGSSPKIDVVVISEA 203
QY 181 SSSNLTDPGCTCTVPEDESEADTVEANFTATFVPSIRQRLNDSGLVTLTDTETVYLMDM 240
DB 204 SSSNLTDPGCTCTVPEDESEADTVEANFTATFVPSIRQRLNDSGLVTLTDTETVYLMDM 263
QY 241 CSPDTISTSTVDTKLSPFCOLSTHDEMNYDYLOSLKYYGAGNPLGPTOGVYANEL 300
DB 264 CSPDTISTSTVDTKLSPFCOLSTHDEMNYDYLOSLKYYGAGNPLGPTOGVYANEL 323
QY 301 IARLTHSPVEDTSSNHTLDDSPATPPLNSTLYADFSDNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVEDTSSNHTLDDSPATPPLNSTLYADFSDNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITOTDGFSSAMTVFASRLYVEMMQCAEQSPPLVRLVNDRVVPLHSCFVDALOR 420
DB 384 TTVENITOTDGFSSAMTVFASRLYVEMMQCAEQSPPLVRLVNDRVVPLHSCFVDALOR 443
QY 421 CTRDSFVRG-SFARSGGDWAECSA 444
DB 444 CTRDSFVRG-SFARSGGDWAECSA 467

RESULT 14
US-08-374-652C-2
; Sequence 2, Application US/28374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.C.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```


NAME: REED, GRANT B.
 REGISTRATION NUMBER: 41,264
 REFERENCE/DOCKET NUMBER: 1050.071001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-38-374-652C-2

Query Match 98.1%; Score 2280; DB 2; Length 467;
 Best Local Similarity 97.3%; Pred. No. 4.2e-228;
 Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASRNSCCTVDCGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 24 ASRNSCTCTVDCGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
 QY 61 ARYPTDSKGGKYSALIEEIQCNATTFDGKYAFKTYNSLIGADDLTPFGCEQLVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEEIQCNATTFDGKYAFKTYNSLIGADDLTPFGCEQLVNSGKIF 143
 QY 121 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 180
 DB 144 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 203
 QY 181 SSSNNTLCPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVTVLMDM 240
 DB 204 SSSNNTLCPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVTVLMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS,KKYVGHGAGNPLGPTCGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS,KKYVGHGAGNPLGPTCGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITOTGFSANVTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPJHGCPEVDALGR 420
 DB 384 TTVENITOTGFSANVTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPJHGCPEVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

RESULT 15
 US-09-155-855-3
 Sequence 3, Application: US/09155855
 Patent No. 6139902
 GENERAL INFORMATION:
 APPLICANT: KONDO, Hiemasa
 APPLICANT: ANAZAWA, Hiemaru
 APPLICANT: KANEKO, Syun-ichi
 APPLICANT: NAGASHIYA, Tadashi
 APPLICANT: TANGE, Tatsuya
 TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 FILE REFERENCE: 61356/124
 CURRENT APPLICATION NUMBER: US/09/155,855
 CURRENT FILING DATE: 1998-10-05
 EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 EARLIER FILING DATE: 1997-04-04
 EARLIER APPLICATION NUMBER: JP 084314
 EARLIER FILING DATE: 1996-04-05
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 3

LENGTH: 467
 TYPE: PRT
 ORGANISM: Aspergillus niger
 US-09-155-855-3

Query Match 96.8%; Score 2259; DB 3; Length 467;
 Best Local Similarity 95.3%; Pred. No. 6.8e-225;
 Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNSCCTVDCGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 24 ASRNSCTCTVDCGYQCFSETSHLWGQYAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
 QY 61 ARYPTDSKGGKYSALIEEIQCNATTFDGKYAFKTYNSLIGADDLTPFGCEQLVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEEIQCNATTFDGKYAFKTYNSLIGADDLTPFGCEQLVNSGKIF 143
 QY 121 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 180
 DB 144 YQRYESLTRNIVPFISSGSSSRVIAAGKXPIEGFQSTKLKDPRAQPGQSSPKIDVWVSEA 203
 QY 181 SSSNNTLCPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVTVLMDM 240
 DB 204 SSSNNTLCPGCTVFEQSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTETVTVLMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS,KKYVGHGAGNPLGPTCGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCCLFTHDEWINDYLOS,KKYVGHGAGNPLGPTCGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITOTGFSANVTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPJHGCPEVDALGR 420
 DB 384 TTVENITOTGFSANVTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPJHGCPEVDALGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECPA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECPA 467

Search completed: November 12, 2003, 14:33:54
 Job time : 22 secs

GenCore version 5.1.6
Copyright: (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw mode.

Run on: November 12, 2003, 14:25:45 : Search time 46 Seconds
(without alignments)
1532.056 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334

Sequence: 1 ASRNQSSCDTVQGVOCFSE.....SFVRLSPARSGDWACFA 444

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_19Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1983.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	448	23	ABE83811 Aspergillus niger
2	2334	100.0	449	22	AAV69547 Aspergillus niger
3	2334	100.0	467	12	AA11333 Recombinant chromo
4	2334	100.0	467	18	AAW15124 Aspergillus ficuum
5	2334	100.0	467	20	AAV39904 A. ficuum phytase
6	2334	100.0	467	23	ABE83810 Aspergillus niger
7	2334	100.0	482	22	AAV72978 Carrot extensin le
8	2322	99.5	467	12	AA113360 Phytase, Aspergil
9	2321	99.4	441	21	AA20505 Aspergillus niger

19	2321	99.4	441	21	AAV69548 Aspergillus niger
20	2291	98.2	441	21	AAV69547 Aspergillus niger
21	2290	98.1	467	15	AA461952 Phytase, Aspergi.
22	2290	98.1	467	15	AA46234 A. niger phytase.
23	2288	98.0	441	21	AA205034 Aspergillus niger
24	2277	97.6	441	21	AA205034 Aspergillus niger
25	2277	97.6	441	21	AAV69546 Aspergillus niger
26	2253	96.5	449	22	AAV72973 Aspergillus niger
27	2253	96.5	482	22	AAV72977 Carrot extensin le
28	2252	96.5	467	16	AAW36500 Aspergillus niger
29	2232	82.8	467	20	AAV43172 Consensus phytase
30	1932	82.8	467	21	AAV69571 Phytase-7, a deriv
31	1932	82.8	457	22	AAU02113 Consensus phytase
32	1929	82.6	467	21	AA205029 Consensus phytase
33	1833	78.5	457	20	AAV43169 Consensus phytase
34	1833	78.5	467	21	AA20326 Mutant phytase-1,
35	1833	78.5	467	21	AAV69568 Consensus phytase
36	1828	78.3	467	21	AAU02110 Consensus phytase
37	1826	78.2	467	22	AAU03005 Consensus phytase
38	1826	78.2	467	22	AAU03017 Consensus phytase
39	1825	78.2	467	22	AAU03004 Consensus phytase
40	1825	78.2	467	22	AAU03010 Consensus phytase
41	1824	78.1	467	22	AAU03007 Consensus phytase
42	1824	78.1	467	22	AAU03009 Consensus phytase
43	1824	78.1	467	22	AAU03025 Consensus phytase
44	1824	78.1	467	22	AAU03023 Consensus phytase
45	1823	78.1	467	22	AAU02119 Consensus phytase
46	1823	78.1	467	22	AAU03011 Consensus phytase
47	1823	78.1	467	22	AAU03040 Consensus phytase
48	1822	78.1	467	21	AA205032 Consensus phytase
49	1822	78.1	467	22	AAU03003 Consensus phytase
50	1822	78.1	467	22	AAU03008 Consensus phytase
51	1822	78.1	467	22	AAU03027 Consensus phytase
52	1822	78.1	467	22	AAU03028 Consensus phytase

ALIGNMENTS

RESULT :

ABE83811

10 ABE83811: standard; Protein: 448 AA.

AC ABE83811:

XX 17-SEP-2002 (first entry)

XX Aspergillus niger phyA related polypeptide 2.

XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.

XX Aspergillus niger.

XX CN333363-A.

XX 30-JAN-2002.

XX 12-JUL-2000; 2000CN-0117245.

XX 12-JUL-2000; 2000CN-0117245.

XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX Chen Z, Yang L, Fang L;

XX WPI; 2002-305615/35.

XX N-PSDB; ABN85590.

XX Phytase gene sequence and application in yeast thereof -

XX Disclosure; Fig 4; 48pp; Chinese.

PS

```
XX The invention relates to a coded phytase gene sequence suitable for
CC secretion and expression in yeast and its application. It is mainly
CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
CC total length structure gene sequence, removing Aspergillus niger signal
CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
CC signal peptide code sequence suitable for secretion and expression at 5'
CC end and connecting a restriction endonuclease site at 3' end. The
CC different carriers can be connected into said gene sequence so as to form
CC a recombinant plasmid with different functions and after the recombinant
CC plasmid using pPIC2 alpha A as carrier is converted into Pasteur Pichia
CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
CC (CCACC NC:M20005) can be obtained through the screening process.
CC By using the invention the industrial process of phytase bio-expression
CC can be successfully implemented. The present sequence is that of a
CC polypeptide of the invention.
XX Sequence 448 AA;
SQ
Query Match 100.0%; Score 2334; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. NC. 2.4e-214;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASRNSQSCDVTDDGYQCFSETSHLMGOYAPFFSLANESVISPVEAGGCRVTPAQVLSRHG 50
Cb 5 ASRNSQSCDVTDDGYQCFSETSHLMGOYAPFFSLANESVISPVEAGGCRVTPAQVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFLLKTYNYSLGADDLTPFGQELVNSGKFK 120
Cb 65 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFLLKTYNYSLGADDLTPFGQELVNSGKFK 124
QY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDWVISEA 180
Cb 125 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDWVISEA 184
QY 181 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 240
Cb 185 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 244
QY 241 CSFDTISTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYANEL 300
Cb 245 CSFDTISTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYANEL 304
QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Cb 305 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 364
QY 361 TTVENITQTDGFSAMTVFPASRLYVEMMCOQAEQEPVLRVLVDRVPLHGCPCVDALGR 420
Cb 365 TTVENITQTDGFSAMTVFPASRLYVEMMCOQAEQEPVLRVLVDRVPLHGCPCVDALGR 424
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Cb 425 CTRDSFVRGLSFARSGGDWAECEFA 448
RESULT 2
AAV72974
ID AAV72974 standard; Protein; 449 AA.
XX
AC AAV72974;
XX
XX AAV72974;
XX
DT 13-JUN-2001 (first entry)
XX
DE Aspergillus niger phytase (Phy) A-1 protein.
XX
KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate.
XX
OS Aspergillus niger.
XX
PN WO200122806-A1.
```

```
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000CWO-AU01183.
XX
XX 24-SEP-1999; 99AU-0003049.
XX
XX (CSIR : COMMONWEALTH SCI & IND RES ORG.
XX (AUMC-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX
XX Richardson AE, Hayes JE, Simpson RJ;
XX WP.; 2001-244964/25.
XX R-FSD3; AAD03283.
XX
XX New isolated nucleic acid encoding a mature phytase polypeptide for
XX enhancing the phosphorus nutrition of a plant, the growth of a plant on
XX a phosphorus source and the phosphorus content of a plant.
XX
XX Claim 6; Page 124-126; 144pp; English.
XX
XX The invention relates to a method of modifying plant productivity
XX which involves expressing (Phy) A phytase gene from Aspergillus niger,
XX in a plant cell. Phytase gene is capable of facilitating plants
XX ability to utilise soil phosphorus. It is used to enhance the
XX phosphorus nutrition of a plant or the growth of a plant on a
XX phosphorus source comprising phytate and/or increase the
XX phosphorus content of a plant. This gene is used to enhance
XX the biomass produced by a plant and also to enhance the rate
XX of hypocotyl production of the rate of epicotyl production.
XX Transgenic plant containing phytase gene has improved productivity
XX than its isogenic counterparts.
XX The present sequence is Aspergillus niger Phy A-1 protein.
XX
XX Sequence 449 AA;
Query Match 100.0%; Score 2334; DB 22; Length 449;
Best Local Similarity 100.0%; Pred. NC. 2.5e-214;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASRNSQSCDVTDDGYQCFSETSHLMGOYAPFFSLANESVISPVEAGGCRVTPAQVLSRHG 60
Cb 5 ASRNSQSCDVTDDGYQCFSETSHLMGOYAPFFSLANESVISPVEAGGCRVTPAQVLSRHG 65
QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFLLKTYNYSLGADDLTPFGQELVNSGKFK 120
Cb 65 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFLLKTYNYSLGADDLTPFGQELVNSGKFK 125
QY 121 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDWVISEA 180
Cb 125 YORYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQCGQSSPKIDWVISEA 185
QY 181 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 240
Cb 185 SSSNNTLDPGTCTVFEDSELADTVANFTATFVPSIRQRLENLDSGVTLTDETVYLMDM 245
QY 241 CSFDTISTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYANEL 300
Cb 245 CSFDTISTSTVDTKLSPPFCDLFTHDEWINYDYQLSLKKYVGHGAGNPLGFTQGVGYANEL 305
QY 301 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
Cb 305 IARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLST 365
QY 361 TTVENITQTDGFSAMTVFPASRLYVEMMCOQAEQEPVLRVLVDRVPLHGCPCVDALGR 420
Cb 365 TTVENITQTDGFSAMTVFPASRLYVEMMCOQAEQEPVLRVLVDRVPLHGCPCVDALGR 425
QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
Cb 425 CTRDSFVRGLSFARSGGDWAECEFA 449
```

```

RESULT 3
AAR11333
ID AAR11333 standard; Protein: 467 AA.
XX
AC AAR11333;
XX
DT 25-MAR-2003 (updated)
DT 30-MAR-2000 (revised)
DT 31-MAY-1991 (first entry)
XX
DE Recombinant chromosomal phytase.
XX
KW Microbial phytase; animal feeds; inositol; inorganic phosphates.
XX
OS synthetic.
XX
PN EP420358-A.
XX
PD 03-APR-1991.
XX
PF 27-SEP-1990; 90EP-0202565.
XX
PR 17-AUG-1990; 90EP-020231.
PR 27-SEP-1989; 89EP-0202436.
PR 27-SEP-1990; 90EP-0202565.
XX
PA (KCNM) GIST-BROCADES NV.
PA (STAM) DSM NV.
XX
PI Van Gorcom RF, Van Hartingsveldt W, Vangatidon PA, Beenstra AE;
PI Luiten RG, Sellen GCM;
XX
WP1: 1991-095799/14.
CR N-PSDB; AAO11175.
XX
DNA encoding phytase - used for recombinant expression for production
PT of phytase for conversion of phytate to inositol and inorganic
PT phosphate esp. in animal feed
XX
PS Disclosure: Fig 8; filpp; English.
XX
This sequence is encoded by a DNA sequence deduced from comparisons of
CC respective sequences of clones identified using oligonucleotide probes.
CC The use of recombinant DNA methods for the enzyme prodn allows the
CC large scale prodn. of proteins and peptides having phytase activity.
CC These are used for the conversion of phytate to inositol and inorganic
CC phosphate and can be used in industrial processes. The phosphate content
CC of manure thus can be decreased. See also AAO11157-74.
CC (Revised record issued to correct errors present in the sequence
CC portion of the original GENESEQ entry.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 23-MAR-2003 to correct PT field.)
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 2334; DB 12; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 444; Conservative C; Mismatches C; Indels 3; Gaps 0;
QY 1 ASRNGSSCCTVDCGYOCFSETSHLKGQYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 60
Db 24 ASRNGSSCCTVDCGYOCFSETSHLKGQYAPFFSLANESVISPEVPAGCRVTFPAQVLSRHG 83
QY 61 ARYPDTSKKKYSALTEETIQNATTFDGKYAFLEKTYNNSLGLADLTPGEQELVNSG:KF 120
Db 84 ARYPDTSKKKYSALTEETIQNATTFDGKYAFLEKTYNNSLGLADLTPGEQELVNSG:KF 143
QY 121 YQRYESLJTRNIVPFFIRSSGSSRVIASGKFFIEGFQSTKJKOPRACPGGSSPKIDVWISGA 180
Db 144 YQRYESLJTRNIVPFFIRSSGSSRVIASGKFFIEGFQSTKJKOPRACPGGSSPKIDVWISGA 203
QY 181 SSSNNTLDGCTCTVDFEDSELADTVANFTATVPFSIRQRLNDLSGVTLTDEVTYLYDM 240

```

RESULT 4

```

AAM15124
ID AAM15124 standard; Protein: 467 AA.
XX
AC AAM15124;
XX
DT 25-MAR-2003 (updated)
DT 21-AUG-1997 (first entry)
XX
DE Aspergillus ficuum phytase.
XX
KW Phytase; phytate; inositol; animal feed.
XX
OS Aspergillus ficuum NRRL 3135.
XX
PE Key Location/Qualifiers
PT Peptide 1..23
XX /label= Sig_peptide
PN EP779037-A1.
XX
PT 18-JUN-1997.
XX
PR 27-SEP-1990; 96EP-0202943.
XX
PR 27-SEP-1989; 89EP-0202436.
PR 17-AUG-1990; 90EP-0202431.
PR 27-SEP-1990; 90EP-0202565.
XX
PA (KCNM) GIST-BROCADES NV.
PA (STAM) DSM NV.
XX
PI Van Paridon PA, Veenstra AE, Luiten RG, Sellen GCM;
PI Van Gorcom RFM, Van Hartingsveldt W;
XX
WP1: 1997-312513/29.
DR N-PSDB; AAT65136; AAT65137.
XX
PT Fungal phytase - releases inorganic phosphate from myo-inositol
PT phosphate, useful to prepare animal feed and reduce phytate levels
XX in manure
PS Example 8; Fig 8; filpp; English.
XX
Aspergillus ficuum phytase (AAM15124) catalyses the conversion of
CC phytate to inositol and inorganic phosphate. It shows optimum
CC activity at pH 5.5 and 2.5, has a specific activity of about 100
CC U/mg and a mol.wt. of 85 kDa (56.5 kDa unglycosylated). Its amino
CC acid sequence was deduced from an isolated phytase cDNA clone
CC (AAT65136). Isolation of this clone allows large-scale prodn. of the
CC phytase in transformed host cells and used to prepare animal feed,
CC reduce phytase levels in manure (by adding the enzyme to animal
CC feed), and also to liberate inorganic phosphates from myo-inositol
CC phosphates in e.g. starch prodn. from cereals and soy processing.

```

CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 467 AA;

Query Match: 100.0%; Score 2334; DB 18; Length: 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-214;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASRNGSSCDTVCGYQCFSETSHLWGOYAPFFSLANESVSEVPAGCRVFAQVLSRHG 60
 DB 24 ASRNGSSCDTVCGYQCFSETSHLWGOYAPFFSLANESVSEVPAGCRVFAQVLSRHG 93
 QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 143
 QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 180
 DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 203
 QY 181 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLENDLSGVTLDTEVTYMDM 240
 DB 204 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLENDLSGVTLDTEVTYMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGAGNPLGFGGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGAGNPLGFGGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDGFSSAWTVPFASRLYVEMWMCQAEQEPPLVRLVNDRVVPLHGCVPDAJGR 420
 DB 384 TTVENITQTDGFSSAWTVPFASRLYVEMWMCQAEQEPPLVRLVNDRVVPLHGCVPDAJGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 5

AA39904
 ID AA39904 standard; Protein: 467 AA.
 AC AA39904;
 XX

DT 07-DEC-1999 (first entry)

XX A. ficum phytase protein sequence.

DE Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW Phytate level reduction; animal manure; food preparation;
 KW soy processing; inositol manufacture.

XX Aspergillus ficum.

XX WC9549022-A1.

PD 30-SEP-1999.

XX 22-MAR-1999; 99NO-DK00153.

XX 23-MAR-1998; 98DK-00004C7.

PR 19-JUN-1998; 98DK-00008C6.

PR 18-SEP-1998; 98DK-0001176.

PR 22-JAN-1999; 99DK-0000091.

XX (NOVO) NOVO-NORDISK AS.

XX

PI Svendsen A;

XX WP; 1999-580444/49.
 DR N-PSDB; AA227421.
 XX

PT New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations -
 XX

Claim 19; Fig 11; 141pp; English.

XX This sequence represents the Aspergillus ficum phytase sequence.
 CC The invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate,
 CC from corn, reaction rate, phytase degradation rate and end level of
 CC released phosphate reached.

XX SQ Sequence 467 AA;

Query Match: 100.0%; Score 2334; DB 20; Length 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-214;
 Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASRNGSSCDTVCGYQCFSETSHLWGOYAPFFSLANESVSEVPAGCRVFAQVLSRHG 60
 DB 24 ASRNGSSCDTVCGYQCFSETSHLWGOYAPFFSLANESVSEVPAGCRVFAQVLSRHG 83
 QY 61 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 120
 DB 84 ARYPTDSKGGKYSALIEEIQONATTFDGKYAFUKTYNYSLGADLTTPGECELVNSGKIF 143
 QY 121 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 180
 DB 144 YORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKOPRAQFGOSSPKIDWVISEA 203
 QY 181 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLENDLSGVTLDTEVTYMDM 240
 DB 204 SSSNNTLDPGTCTVFEDESLEADTVEANFTATFVPSRQRLENDLSGVTLDTEVTYMDM 263
 QY 241 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGAGNPLGFGGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPPFCDLTFHDEWINDYLSKYYGAGNPLGFGGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 383
 QY 361 TTVENITQTDGFSSAWTVPFASRLYVEMWMCQAEQEPPLVRLVNDRVVPLHGCVPDAJGR 420
 DB 384 TTVENITQTDGFSSAWTVPFASRLYVEMWMCQAEQEPPLVRLVNDRVVPLHGCVPDAJGR 443
 QY 421 CTRDSFVRGLSFARSGGDWAECEFA 444
 DB 444 CTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 6

AB83810
 ID AB83810 standard; Protein: 467 AA.
 AC AB83810;
 XX

XX 17-SEP-2002 (first entry)

DT

Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 39 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 98
 QY 61 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPFKTYNYSLGADDLTPFGEQELVNSGKIF 120
 DB 99 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPFKTYNYSLGADDLTPFGEQELVNSGKIF 158
 QY 121 YORYESLTKNIVFFIRSGSSRVIASGKKFIEGOSTKLDRAQPCSSPKIDVWVSEA 180
 DB 159 YORYESLTKNIVFFIRSGSSRVIASGKKFIEGOSTKLDRAQPCSSPKIDVWVSEA 218
 QY 181 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVTLTDTEVTYLYDM 240
 DB 219 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVTLTDTEVTYLYDM 278
 QY 241 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 300
 DB 279 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 338
 QY 301 IARLTHSPVHDDTSSNHTLDSSTPATFPLNSTLYADFSDHNGIISILFALGLVNGTKPLST 360
 DB 339 IARLTHSPVHDDTSSNHTLDSSTPATFPLNSTLYADFSDHNGIISILFALGLVNGTKPLST 398
 QY 361 TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCVPDLAGR 420
 DB 399 TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCVPDLAGR 458
 QY 421 CTRDSFVRLGSLFARSOGDWAECFA 444
 DB 459 CTRDSFVRLGSLFARSOGDWAECFA 482

RESULT 8
 AAR14362
 ID AAR14360 standard; Protein: 467 AA.

AC AAR14360;
 XX
 DT 25-MAR-2003 (updated)
 DT 09-DEC-1991 (first entry)
 XX
 DE Phytase.
 XX
 KW Transgenic plants; inositol.
 XX
 OS Aspergillus ficium strain NRRJ 3135.
 XX
 FH Key
 FT Peptide 1..23 Location/Qualifiers
 FT /note= "signal peptide"
 FT 24..444
 FT /note= "mature peptide"

XX EP449375-A.
 XX
 XX 02-OCT-1991.
 XX
 XX 25-MAR-1991; 91EP-0200687.
 XX
 XX 21-SEP-1990; 90US-0586765.
 XX 23-MAR-1990; 90US-0498561.
 XX
 XX (KONN) GIST-BROCADES NV.
 XX (MOGE-) MOGEN INT NV.
 XX (STAK) DSM NV.
 XX
 XX Pen J, Hoekema A, Sijmons PC, Vanocoyen Acc, Rietveld X;
 XX Verwoerd TC;
 XX WPI: 1991-289814/40.
 DR

DR N-PSDB; AAQ13878.
 XX
 PT Phytase prodn. transgenic plants or plant organs - used in e.g.
 PT foods or feedstuffs for prodn. of inositol and inorganic
 PT phosphate from phytate.
 XX
 PS Disclosure; Fig 2; 28pp; English.
 XX
 CC The amino acid sequence codes for phytase which catalyses the
 CC conversion of phytate to inositol and inorganic phosphorus. The
 CC phytase given here, obtd. from Aspergillus ficuum, has been
 CC determined to possess one of the highest levels of specific
 CC activity as well as having better thermostability than phytases
 CC produced by other microorganisms. It can also be used as a feed
 CC additive for non-ruminants to promote growth and also to reduce
 CC the phosphorus content of animal manure. It may also be used in
 CC e.g. soy processing, in the starch and fermentation industries and
 CC in steeping of corn or sorghum kernels. See also EP-449376.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 467 AA;

Query Match 99.5%; Score 2122; DB 12; Length 467;
 Best Local Similarity 99.5%; Pred. No. 3.7e-213;
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 60
 DB 24 ASRNQSSCCTVDOGYCCFSETSHLWGOVAPFFSLANESVISEVPAGCRVTFAQVLSRHG 83
 QY 61 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPFKTYNYSLGADDLTPFGEQELVNSGKIF 120
 DB 94 ARYPDTSKGGKYSALIEEIQONATTFDQKYAPFKTYNYSLGADDLTPFGEQELVNSGKIF 143
 QY 121 YORYESLTKNIVFFIRSGSSRVIASGKKFIEGOSTKLDRAQPCSSPKIDVWVSEA 180
 DB 144 YORYESLTKNIVFFIRSGSSRVIASGKKFIEGOSTKLDRAQPCSSPKIDVWVSEA 203
 QY 181 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVTLTDTEVTYLYDM 240
 DB 204 SSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRORLENDLSGVTLTDTEVTYLYDM 263
 QY 241 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 300
 DB 264 CSFDTISTSTVDTKLSPFCDLTHDEWINYDLSLKKYKYGAGNPLGPTQGVGYANEL 323
 QY 301 IARLTHSPVHDDTSSNHTLDSSTPATFPLNSTLYADFSDHNGIISILFALGLVNGTKPLST 360
 DB 324 IARLTHSPVHDDTSSNHTLDSSTPATFPLNSTLYADFSDHNGIISILFALGLVNGTKPLST 383
 QY 361 TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCVPDLAGR 420
 DB 384 TTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCVPDLAGR 443
 QY 421 CTRDSFVRLGSLFARSOGDWAECFA 444
 DB 444 CTRDSFVRLGSLFARSOGDWAECFA 467

RESULT 9
 AAR20505
 ID AAR20505 standard; Protein: 441 AA.
 XX
 AC AAR20505;
 XX
 DT 05-DEC-2000 (first entry).
 XX
 DE Aspergillus niger NRRJ3-35 phytase SEQ ID NO:5.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;

KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 XX Aspergillus niger.
 XX WO200043503-A1.
 XX PN
 XX PD
 XX 27-JUL-2000.
 XX PF
 XX 21-JAN-2000; 2000WO-DK00025.
 XX PR
 XX 22-JAN-1999; 99DK-0000092.
 XX PR
 XX 21-SEP-1999; 99DK-0001340.
 XX FA
 XX (NOVO) NOVO NORDISK AS.
 XX PI
 XX Lehmann M;
 XX DR
 XX WPI; 2000-49:161/43.
 XX XX
 XX Novel phytases with improved properties such as temperature stability,
 XX pH stability and substrate specificity, for use in pharmaceuticals and
 XX compound foods and feeds -
 XX PT
 XX PS
 XX Example 1; Fig 1a-d; 240pp; English.
 XX CC
 XX The present invention describes improved phytases, preferably with
 XX increased thermostability, and methods for producing them. The methods
 XX can be used for producing phytases with improved properties e.g.
 XX temperature stability, pH stability, pH profile, temperature profile,
 XX specific activity, substrate specificity, substrate cleavage pattern,
 XX substrate binding, position specificity, the velocity and level of
 XX release of phosphate from corn, reaction rate, phytate degradation rate,
 XX and end level of released phosphate. The phytases can be used to produce
 XX pharmaceutical compositions or compound food or feeds. The feed can be
 XX used to reduce levels of phytate in animal manure, by converting it
 XX into lower inositol phosphates and/or inositol and inorganic phosphate.
 XX The present sequence represents a phytase sequence from the present
 XX invention.
 XX CC
 XX XX
 XX SQ

Qy	4	NQSSCOTVCGGQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQLSRHGARY	63
Db	1	NQSSCOTVCGGQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQLSRHGARY	60
Qy	64	PTDSKGGKYSALFEIQONATTFDGKVAFLKTNYSAGADLTPFGSQELWNGIKFYQR	123
Db	61	PTDSKGGKYSALFEIQONATTFDGKVAFLKTNYSAGADLTPFGSQELWNGIKFYQR	120
Qy	124	YESLRNIVPFRSSGSRVIASSKKIEGQSTKDEPRAQCGSSPKIDWISASSS	183
Db	121	YESLRNIVPFRSSGSRVIASSKKIEGQSTKDEPRAQCGSSPKIDWISASSS	180
Qy	184	NNTLPDGTCTVFDESELAQTVANFTATFVPSIRQRLENLDSGVTLTDTETVLYMCMCSF	243
Db	181	NNTLPDGTCTVFDESELAQTVANFTATFVPSIRQRLENLDSGVTLTDTETVLYMCMCSF	240
Qy	244	DTISTSTVCTVGLSPFCDLFTDEINVDYJLSLAKKYYGHGAGNPLGTCQGVGANELIAR	303
Db	241	DTISTSTVCTVGLSPFCDLFTDEINVDYJLSLAKKYYGHGAGNPLGTCQGVGANELIAR	300
Qy	304	LTHSPVMDTSSNHTLDSSPATEP-NSTLYADFSDHNGIISILFALGLYNGEKPLSTTV	363
Db	301	LTHSPVMDTSSNHTLDSSPATEP-NSTLYADFSDHNGIISILFALGLYNGEKPLSTTV	360
Qy	364	ENITQDGFSSAWTVPFASRLYVEMMOCAQOEPLVLRVNDRVVPLHGGCPVDALGCTR	423
Db	361	ENITQDGFSSAWTVPFASRLYVEMMOCAQOEPLVLRVNDRVVPLHGGCPVDALGCTR	420

Query Match 99.4%; Score 2321; DB 21; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4, 2e-213;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 DSFVRGLSFARSGGDNAECFA 444
 Db 421 DSFVRGLSFARSGGDNAECFA 441

RESULT 10
 AAY69548
 ID AAY69548 standard; protein; 441 AA.
 XX AC AAY69548;
 XX DT 19-APR-2000 (first entry)
 XX DE Aspergillus niger strain NRRL3135 mature phytase.

KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability.

XX OS Aspergillus niger str. NRRL3135.
 XX PN EP989083-A1.
 XX XX
 XX PD 05-JAN-2000.
 XX XX
 XX PF 23-JUN-1999; 99EP-0111949.
 XX PR 29-JUN-1998; 98EP-0111960.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Brugger R, Lehmann M, Wyss M;
 XX DR WPI; 2000-099429/09.

XX New stabilized enzyme formulation, useful for feed compositions for
 XX monogastric animals -
 XX FS Example 3; Fig 13; 101pp; English.

XX The invention relates to a novel stabilised dry or liquid enzyme
 XX formulation, comprising phytase (myo-inositol hexakisphosphate
 XX phosphohydrolase) and one or more stabilising agents including
 XX xylitol or ribitol; polyethylene glycols with a molecular weight of 600
 XX to 1000 Da; preferably 1000 to 3350 Da; the disodium salts of malonic,
 XX glutaric and succinic acid; carboxymethyl-cellulose; and sodium alginate.
 XX The stabilised phytase formulation is used in a method for preparing a
 XX feed composition for monogastric animals (e.g., pigs, poultry) and
 XX provides a monogastric animal with its dietary requirements of
 XX phosphorus. Although a large amount of phosphate is present in animal
 XX feed in the form of phytate phosphorus, monogastric animals are unable
 XX to utilise this form of phosphate, resulting in the addition of extra
 XX phosphate to the feed of such animals. Phytase enhances the nutritional
 XX value of plant material without the need for adding additional phosphate
 XX to the feed. The level of phosphate pollution in the environment is
 XX reduced by adding phytase to animal feed, as the animal can make use of
 XX the inorganic phosphate liberated from phytate phosphorus using the
 XX enzyme. The phytase formulation of the invention has an improved
 XX thermostability and can therefore remain stable during long-term storage
 XX and can withstand feed processing methods such as extrusion, expansion
 XX and pelleting. Sequences AAY69544-Y69556 represent the amino acid
 XX sequences of mature phytases from a variety of fungi (mainly different
 XX strains of Aspergillus species), which were used in an exemplification of
 XX the present invention to determine a consensus phytase sequence.
 XX designated phytase-1 (AAY69558). An initial consensus sequence, AAY69557,
 XX was determined using the program PRETTY, and the phytase-1 consensus
 XX derived from the initial consensus. Consensus phytase sequences were
 XX produced in the exemplifications, as a prior art consensus phytase
 XX sequence was found to have higher thermal stability than native
 XX phytases.

XX Sequence 441 AA;

```

Query Match      99.4%; Score 2321; DB 21; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2e-213;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cc 4 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 63
Cc 1 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 60
Cc 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
Cc 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
Cc 124 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 183
Cc 121 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 180
Cc 184 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 243
Cc 181 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 240
Cc 244 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 303
Cc 241 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 300
Cc 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
Cc 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
Cc 364 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 423
Cc 361 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 420
Cc 424 DSFVRGLSFARSGGDWAECEFA 444
Cc 421 DSFVRGLSFARSGGDWAECEFA 441

Query Match      99.4%; Score 2291; DB 21; Length 441;
Best Local Similarity 98.0%; Pred. No. 3.1e-210;
Matches 432; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Cc 4 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 63
Cc 1 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 60
Cc 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
Cc 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
Cc 124 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 183
Cc 121 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 180
Cc 184 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 243
Cc 181 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 240
Cc 244 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 303
Cc 241 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 300
Cc 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
Cc 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
Cc 364 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 423
Cc 361 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 420
Cc 424 DSFVRGLSFARSGGDWAECEFA 444
Cc 421 DSFVRGLSFARSGGDWAECEFA 441

RESULT 12
AAR46792
ID AAR46792 standard; protein; 441 AA.
XX
AC AAV69547;
CC
CC 19-APR-2000 (first entry)
DE
DE Aspergillus niger T213 mature phytase.
XX
XX Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
XX thermostable; animal feed; monogastric animal; phytate phosphorus;
XX phosphate availability.
XX
XX Aspergillus niger T213.
XX
XX EP969089-A1.
XX
XX 05-JAN-2003.
XX
XX 23-JUN-1999; 98EP-0111949.
XX
XX 29-JUN-1998; 98EP-0111960.
XX
XX (HOPF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brugger R, Lehmann M, Wyss M;
XX
XX WPI; 2000-099429/09.
XX
XX New stabilized enzyme formulation, useful for feed compositions for
XX monogastric animals.
XX
XX Example 3; Fig 13; 101pp; English.
XX

```

```

Cc The invention relates to a novel stabilised dry or liquid enzyme
Cc formulation, comprising phytase (myo-inositol hexakisphosphate
Cc phosphohydrolase) and one or more stabilising agents including
Cc xylitol or ribitol; polyethylene glycols with a molecular weight of 600
Cc to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of alonic,
Cc glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
Cc The stabilised phytase formulation is used in a method for preparing a
Cc feed composition for monogastric animals (e.g., pigs, poultry) and
Cc provides a monogastric animal with its dietary requirements of
Cc phosphorus. Although a large amount of phosphate is present in animal
Cc feed in the form of phytate phosphorus, monogastric animals are unable
Cc to utilise this form of phosphate, resulting in the addition of extra
Cc phosphate to the feed of such animals. Phytase enhances the nutritional
Cc value of plant material without the need for adding additional phosphate
Cc to the feed. The level of phosphate pollution in the environment is
Cc reduced by adding phytase to animal feed, as the animal can make use of
Cc the inorganic phosphate liberated from phytate phosphorus using the
Cc enzyme. The phytase formulation of the invention has an improved
Cc thermostability and can therefore remain stable during long-term storage
Cc and can withstand feed processing methods such as extrusion, expansion
Cc and pelleting. Sequences AAV69544-Y69556 represent the amino acid
Cc sequences of mature phytases from a variety of fungi (mainly different
Cc strains of Aspergillus species), which were used in an exemplification of
Cc the present invention to determine a consensus phytase sequence,
Cc designated phytase-1 (AAV69558). An initial consensus sequence, AAV69557,
Cc was determined using the program PRETTY, and the phytase-1 consensus was
Cc derived from the initial consensus. Consensus phytase sequences were
Cc produced in the exemplifications, as a prior art consensus phytase
Cc sequence was found to have higher thermal stability than native
Cc phytases.
Cc
XX
SQ Sequence 441 AA;

```

```

Query Match      98.2%; Score 2291; DB 21; Length 441;
Best Local Similarity 98.0%; Pred. No. 3.1e-210;
Matches 432; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Cc 4 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 63
Cc 1 NOSSCDTDCGQCSETSHLWGYAFPSLANESVISPVPAGCRVTFQAQVLSRHGARY 60
Cc 64 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 123
Cc 61 PTDSKGGKYSALIEEIQONATTFDGKYAFKTYNYSLGADLTFFGQELVNSGKIFYOR 120
Cc 124 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 183
Cc 121 YESLTRNIVPFRSSGSRVSIASGKFIQFQSTKLKDPRAQPGQSSPKIDVISEASS 180
Cc 184 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 243
Cc 181 NNTLDPGTCTVFESSEADTVEANFTATFVPSIRORLENDLSGVTLTDEVTYVMDMCSF 240
Cc 244 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 303
Cc 241 DTISTSTVDTKLSPFCDLTFFHDEWNYDYJQSLKYYGHGAGNPLJPTQGVGVANELIAR 300
Cc 304 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 363
Cc 301 LTHSPVHDDTSSNHTLDSSPA:FPPLNSTLYADFSHONGIISILFALGLYNGTKPJSTTV 360
Cc 364 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 423
Cc 361 ENITQTDGFSSAWTVFASRLVYVEMMOCQAEPLVRLVNDRVVPLHGCPVDALGRCTR 420
Cc 424 DSFVRGLSFARSGGDWAECEFA 444
Cc 421 DSFVRGLSFARSGGDWAECEFA 441

RESULT 12
AAR46792
ID AAR46792 standard; protein; 467 AA.

```

```

XX AC AAR46792;
XX CT 25-MAR-2003 (updated);
XX DT 19-AUG-1994 (first entry);
XX DE Phytase.
XX KW pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;
XX KW phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;
XX KW p-ant; feed composition; filtration.
XX CS Aspergillus niger.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /note= "Signal peptide"
XX FT Protein 20..467
XX FT /note= "Mature phytase"
XX PN W09403612-A1.
XX PD 17-FEB-1994.
XX PF 30-JUL-1993; 93WO-F10310.
XX PR 31-JUL-1992; 92US-0923724.
XX PA (ALCO-) ALKO LTD.
XX PI Cantrell M, Fagerstrom RB, Miettinen-Oinonen ASK;
XX PI Nevalainen HK, Paalheim MT, Piddington C, Rambosek JA;
XX PI Torkkeli TK, Turunen MK;
XX DR WPI; 1994-065700/08.
XX DR N-PSDB; AAC59126.
XX CS Carpers. contg. phytate degrading enzymes - obtd. by expression
XX PT of their genes in Trichoderma, used partic. for producing animal
XX PT feed compens.
XX PS Claim 3; Fig 5; 142pp; English.
XX CS This sequence represents a phytase which was used in the production of
XX CC the composition of the invention. This sequence may be introduced
XX CC into a Trichoderma host which then expresses it and the protein is
XX CC collected from the culture medium. By using Trichoderma as a host
XX CC for Aspergillus phytate degrading enzymes such as this, a totally
XX CC different enzyme composition compared to that secreted from
XX CC Aspergillus results. The enzyme composition can be used for removal
XX CC of phytic acid or inositol hexaphosphoric acid from raw material,
XX CC particularly plant material. The composition is used in feed
XX CC compositions for animals. By using Trichoderma as a source of a
XX CC composition containing phytate degrading enzymes some difficult
XX CC downstream processing problems, eg. filtration, that occur with
XX CC similar Aspergillus compositions are avoided and yields are improved.
XX CC (Updated on 25-MAR-2003 to correct EN field.)
XX SQ Sequence 467 AA;

Query Match 98.1%; Score 2290; DB 15; Length 467;
Best Local Similarity 97.3%; Pred. No. 4.3e-210;
Matches 432; Conservative 8; Mismatches 4; Indels C; Gaps 0;

QY 1 ASRNQSCDTVDQYQCFSETSHLWGQYAPFFSLANESVTSPEVPACRVTFAQVLSRHG 60
DB 1 ASRNQSCDTVDQYQCFSETSHLWGQYAPFFSLANESVTSPEVPACRVTFAQVLSRHG 83
QY 61 ARYETDSKGYKYSALIEICONATFDGKYAFILKTYNYS;GADDLTPFGQELVNSGIKF 120
DB 84 ARYETDSKGYKYSALIEICONATFDGKYAFILKTYNYS;GADDLTPFGQELVNSGIKF 143
QY 121 YORVESLTRNIVPIRSSGSSRVIASGKFEQFQSTKLKDPRAQPGQSSPKIDWVISEA 190

```

RESULT 13

```

AAR46234
CD AAR46234 standard; Protein; 467 AA.
XX AC AAR46234;
XX CT 25-MAR-2003 (updated)
XX DT 01-SEP-1994 (first entry);
XX DE A. niger phytase.
XX KW Phytase; pH 2.5 acid phosphatase; A. niger; strain ALK0243; mineral;
XX KW liberation; phytate; Plant material; feed treatment; animal; inositol;
XX KW enzyme mixture; hydrolysis; phosphate; phytic acid complex.
XX CS Aspergillus niger var. awamori strain ALK0243.
XX FH Key Location/Qualifiers
XX FT Peptide 407..422
XX FT /note= "Peptide #420"
XX PN W09403372-A1.
XX PD 17-FEB-1994.
XX PF 27-JUL-1993; 93WO-US07059.
XX PR 31-JUL-1992; 92US-0925401.
XX PA (ALCO-) ALKO LTD.
XX PA (NEVA/) NEVALAINEN H K M.
XX PA (PANJ-) PANLABS INC.
XX PI Cantrell MA, Fagerstrom RB, Houston CS, Miettinen-Oinonen ASK;
XX PI Palohelmo MT, Piddington CS, Rambosek JA, Turunen MK;
XX DR WPI; 1994-065302/C8.
XX DR N-PSDB; AAQ56944.
XX PT Nucleic acid encoding phytase and pH 2.5 acid phosphatase - used
XX PT to produce the enzymes and enzyme mixts. for liberating minerals
XX PT from phytate, partic. for animal feed
XX PS Claim 1; Fig 9; 103pp; English.
XX CC The sequences given in AAR46234-35 represent the phytase and pH 2.5 acid
XX CC phosphatase from A. niger var. awamori strain ALK0243. The cDNA
XX CC encoding these sequences was used to transformed host cells for the
XX CC expression of the phytase and phosphatase. The phytase and pH 2.5 acid

```

CC phosphatase proteins can be used to liberate minerals from phytates
 CC in plant materials either in vitro, ie, in feed treatment processes,
 CC or in vivo, ie, by administering the enzymes to animals. The
 CC enzymes can be mixed to provide a balanced enzyme mixture in which
 CC cooperative enzyme activity rapidly and effectively catalyses the
 CC near complete hydrolysis of phytate to inositol and free phosphate
 CC with release of minerals from the phytic acid complex.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 467 AA;

Query Match 98.1%; Score 2290; DB 15; Length 467;
 Best Local Similarity 97.3%; Pred. No. 4.3e-210;
 Matches 432; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASRQSSCDTVDQGYCCFSETSHLWGQVAPFFSLANESVISEVPAGCRVTFACVLSRHG 60
 DB 24 ASRQSSCDTVDQGYCCFSETSHLWGQVAPFFSLANESVISEVPAGCRVTFACVLSRHG 83
 QY 61 ARYPTSGKGYKYSALIEEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSGKFP 120
 DB 84 ARYPTSGKGYKYSALIEEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSGKFP 143
 QY 121 YRVESLNRNVPFIRSSGSRVVASGKFEFGQSTKLKDPRAQPGSSFKIDVWVSEA 180
 DB 144 YRVESLNRNVPFIRSSGSRVVASGKFEFGQSTKLKDPRAQPGSSFKIDVWVSEA 203
 QY 181 SSSNNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVYLMQV 240
 DB 204 SSSNNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVYLMQV 263
 QY 241 CSFTTISTVDTKLSFPCDLFTHDEWINDYLSKYYGHGAGNPLGPTQGVYANEL 300
 DB 264 CSFTTISTVDTKLSFPCDLFTHDEWINDYLSKYYGHGAGNPLGPTQGVYANEL 323
 QY 361 LARLTHSPVHDTSSNHTLDSPPATFPLKNTLYADFSDHNGIISILFALGLYNGTKPST 360
 DB 324 LARLTHSPVHDTSSNHTLDSPPATFPLKNTLYADFSDHNGIISILFALGLYNGTKPST 383
 QY 361 TTVENITQDGFSSAWTVFFASRLYVENMQCAQOEPLVRVLRVDRVVPVPLHGCPCDALGR 420
 DB 384 TTVENITQDGFSSAWTVFFASRLYVENMQCAQOEPLVRVLRVDRVVPVPLHGCPCDALGR 443
 QY 421 CTDSFVRLGSLFARSGGDWAECSA 444
 DB 444 CTDSFVRLGSLFARSGGDWAECSA 467

RESULT 14
 AAB20504
 ID AAB20504 standard; Protein: 441 AA.
 XX
 AC AAB20504;
 XX

DS-DEC-2000 (first entry)

Aspergillus niger T23 phytase SEQ ID NO:4.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 temperature stability; pH profile; temperature profile; reaction rate;
 specific activity; substrate specificity; substrate cleavage pattern;
 substrate binding; position specificity; phytate degradation rate;
 food; feed; phytate; manure.

Aspergillus niger.

MO2000043503-A1.

27-JUL-2000.

21-JAN-2000; 2000KC-DK00025.

22-JAN-1999; 99DK-0000092.

FR 21-SEP-1999; 99DK-0001340.

(NOVO) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43.

Novel phytases with improved properties such as temperature stability,
 pH stability and substrate specificity, for use in pharmaceuticals and
 compound foods and feeds -

Example 1: Fig 1a-d; 240pp; English.

The present invention describes improved phytases, preferably with
 increased thermostability, and methods for producing them. The methods
 can be used for producing phytases with improved properties e.g.
 temperature stability, pH stability, pH profile, temperature profile,
 specific activity, substrate specificity, substrate cleavage pattern,
 substrate binding, position specificity, the velocity and level of
 release of phosphate from corn, reaction rate, phytate degradation rate,
 and end level of released phosphate. The phytases can be used to produce
 pharmaceutical compositions or compound food or feeds. The feed can be
 used to reduce levels of phytate in animal manure, by converting it
 into lower inositol phosphates and/or inositol and inorganic phosphate.
 The present sequence represents a phytase sequence from the present
 invention.

Sequence 441 AA;

Query Match: 98.0%; Score 2288; DB 21; Length 441;

Best Local Similarity 97.7%; Pred. No. 6e-210;
 Matches 432; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSSSDTVDQGYCCFSETSHLWGQVAPFFSLANESVISEVPAGCRVTFACVLSRHGARY 63
 DB 1 NSSSDTVDQGYCCFSETSHLWGQVAPFFSLANESVISEVPAGCRVTFACVLSRHGARY 60
 QY 64 PTDSKGYKYSALIEEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSG-KFYOR 123
 DB 61 PTDSKGYKYSALIEEIQONATTFDQKYAFPLKTYNYSLGADDLTPFGCELVNSG-KFYOR 120
 QY 124 YESLNRNVPFIRSSGSRVVASGKFEFGQSTKLKDPRAQPGSSFKIDVWVSEA 183
 DB 121 YESLNRNVPFIRSSGSRVVASGKFEFGQSTKLKDPRAQPGSSFKIDVWVSEA 180
 QY 184 NNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVYLMQCSF 243
 DB 181 NNTLDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDTEVYLMQCSF 240
 QY 244 DTISTVDTKLSFPCDLFTHDEWINDYLSKYYGHGAGNPLGPTQGVYANELIAR 303
 DB 241 DTISTVDTKLSFPCDLFTHDEWINDYLSKYYGHGAGNPLGPTQGVYANELIAR 300
 QY 304 LTHSPVHDTSSNHTLDSPPATFPLKNTLYADFSDHNGIISILFALGLYNGTKPSTTTV 363
 DB 301 LTHSPVHDTSSNHTLDSPPATFPLKNTLYADFSDHNGIISILFALGLYNGTKPSTTTV 360
 QY 364 ENITQDGFSSAWTVFFASRLYVENMQCAQOEPLVRVLRVDRVVPVPLHGCPCDALGRCTR 423
 DB 361 ENITQDGFSSAWTVFFASRLYVENMQCAQOEPLVRVLRVDRVVPVPLHGCPCDALGRCTR 420
 QY 424 DSFVRLGSLFARSGGDWAECSA 444
 DB 421 DSFVRLGSLFARSGGDWAECSA 441

RESULT 15

AAB20503

ID AAB20503 standard; Protein: 441 AA.

XX

AC AAB20503;

XX

05-DEC-2000 (first entry)

Aspergillus niger var. awamori phytase SEQ ID NO:3.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Aspergillus niger var. awamori.

WO200043503-A1.

27-JUL-2000.

21-JAN-2000; 2000WO-DK0025.

22-JAN-1999; 99DK-000092.

21-SEP-1999; 99DK-0001340.

(NOVC) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-49116-/43.

Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds.

Example 1; Fig 1a-d; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present invention.

Sequence 441 AA;

Query Match 97.6%; Score 2277; DB 21; Length 441;

Best Local Similarity 97.3%; Pred. No. 6.8e-209;

Matches 429; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 4 NQSCDTVDQGYQCFSETSLHMGQYAFPPS:ANESVTSPEVPAGCRVTFQGV:SRHGARY 63
DB 1 NQSCDTVDQGYQCFSETSLHMGQYAFPPS:ANESVTSPEVPAGCRVTFQGV:SRHGARY 60

QY 64 PTDSKGGKYSALIEEIQGNATTFGKVAFLKYNYSIGADLTGPGFOELVNSG:KEYCR 123
DB 61 PTESGKKYSALIEEIQGNATTFGKVAFLKYNYSIGADLTGPGFOELVNSG:KEYCR 120

QY 124 YESLTRNIPFIRSGSSRVIASGKKEGFSQSTKJDPRAQPGQSSPKIDVVISASSS 193
DB 12 YESLTRNIPFIRSGSSRVIASGKKEGFSQSTKJDPRAQPGQSSPKIDVVISASSS 180

QY 184 NNTLDPGTCVFESELAADTVEANFTATFVPS:RORLENDLSGVTLDTETVYLMQVCSF 243
DB 181 NNTLDPGTCVFESELAADTVEANFTATFVPS:RORLENDLSGVTLDTETVYLMQVCSF 240

QY 244 DTISTSTVDTKLSFPCDLTFHDEINVDYLSLKKYKHGAGNPLGPTQGVYANELLAR 303
DB 241 DTISTSTVDTKLSFPCDLTFHDEINVDYLSLKKYKHGAGNPLGPTQGVYANELLAR 300

QY 364 LTHSPVHDD:SSNHTLSSSPATFPJNSTLYADPSHENGII:SLFALGLYNGTKPLSTTTV 363
DB 361 LTHSPVHDD:SSNHTLSSSPATFPJNSTLYADPSHENGII:SLFALGLYNGTKPLSTTTV 360
QY 364 ENITOTDGFSSAWTVPFASRLYVEMMOCQABQEP:VRVLVNDRVVPLHGCPVDALGRCTR 423
DB 361 ENITOTDGFSSAWTVPFASRLYVEMMOCQABQEP:VRVLVNDRVVPLHGCPVDALGRCTR 420
QY 424 DSFVRGLSFARSGGQWAECSA 444
DB 421 DSFVRGLSFARSGGQWAECSA 441

Search completed: November 12, 2003, 14:31:26
Job time : 48 secs

GenCore version: 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: November 12, 2003, 14:29:20 ; Search time 19 Seconds
(without alignments)
2937.830 Million cell updates/sec

Title: US-10-062-848-1

Perfect score: 2334
Sequence: 1 ASRNSQSDTVQGYQCFSE.....SFVAGLFARSGGDWASCEFA 444

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMSL_23:

1: sp.archaea:

2: sp.bacteria:

3: sp.fungi:

4: sp.human:

5: sp.invertebrate:

6: sp.mammal:

7: sp.mhc:

8: sp.organelle:

9: sp.phage:

10: sp.plant:

11: sp.recent:

12: sp.virus:

13: sp.unclassified:

14: sp.unclassified:

15: sp.virus:

16: sp.bacteriophage:

17: sp.bacteriophage:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	2294	98.3	467	Q9UJZ7	Q9UJZ7 aspergillus
2	2260	96.8	488	Q8U255	Q8U255 aspergillus
3	2259	96.8	467	Q9UJZ7	Q9UJZ7 aspergillus
4	2249	95.4	467	Q9HEQ3	Q9HEQ3 aspergillus
5	1610	69.0	466	Q9C1T1	Q9C1T1 aspergillus
6	1606.5	68.8	465	Q9C092	Q9C092 aspergillus
7	1605.5	68.8	442	Q8WZ25	Q8WZ25 aspergillus
8	1520	65.1	466	Q9C100	Q9C100 aspergillus
9	1496.5	64.1	466	Q9C096	Q9C096 aspergillus
10	1493	64.0	466	Q9C085	Q9C085 aspergillus
11	1429.5	48.4	487	Q9C107	Q9C107 thelavia h
12	762.5	32.7	443	Q96V75	Q96V75 trameetes pu
13	752.5	32.2	439	Q96VH9	Q96VH9 peniophora
14	739.5	31.7	453	Q96V70	Q96V70 agrocycbe pe
15	739	31.7	442	Q96VK9	Q96VK9 cf. ceripor
16	732	31.4	442	Q96VK8	Q96VK8 cf. ceripor

17	357	15.3	482	3	Q9X1W7	Q9X1W7 monascus an
18	255	15.2	469	3	Q9V846	Q9V846 kluyveromyc
19	302.5	13.0	442	3	Q74677	Q74677 pichia angu
20	300	12.9	463	3	C63172	C63172 schizosacch
21	245	9.6	454	1	Q35217	Q35217 rattus norv
22	216	9.3	467	5	Q9VW72	Q9VW72 drosophila
23	212	9.1	431	11	Q8VDR0	Q8VDR0 mus musculu
24	210	9.0	471	11	Q9Z216	Q9Z216 mus musculu
25	209	9.0	449	13	Q9217C	Q9217C gallus gali
26	234	8.7	487	4	Q95172	Q95172 homo sapien
27	233	8.7	487	4	Q9UW1	Q9UW1 homo sapien
28	232	8.7	467	5	C95421	C95421 drosophila
29	201	8.6	487	4	Q9JGA3	Q9JGA3 homo sapien
30	185.5	7.9	464	13	Q9CXV1	Q9CXV1 fugu rubrip
31	185	7.9	453	5	Q96420	Q96420 drosophila
32	184	7.9	453	5	Q96438	Q96438 drosophila
33	176.5	7.6	497	10	Q94132	Q94132 arabidopsis
34	157	6.7	274	11	Q9CJDS	Q9CJDS mus musculu
35	148	6.3	210	5	Q8T312	Q8T312 drosophila
36	147	6.3	210	5	Q8T312	Q8T312 drosophila
37	142	6.1	606	16	Q8G772	Q8G772 bifidobacte
38	137.5	5.9	198	3	Q9UTX1	Q9UTX1 schizosacch
39	137.5	5.9	374	11	Q9TMS	Q9TMS mus musculu
40	137.5	5.9	418	11	Q8SP40	Q8SP40 mus musculu
41	136.5	5.8	381	11	Q9QXG5	Q9QXG5 mus musculu
42	132.5	5.7	1341	16	Q8EUS5	Q8EUS5 mycoplasma
43	128	5.5	480	11	Q8BZ12	Q8BZ12 mus musculu
44	127	5.4	480	11	Q8BHA9	Q8BHA9 mus musculu
45	120.5	5.2	413	16	Q8XB26	Q8XB26 escherichia

ALIGNMENTS

RESULT 1

Q9UJZ7 PRELIMINARY; PRT; 467 AA.
 AC Q9UJZ7
 DT 01-MAY-2000 (TRMSBLrel. 13, Created:
 DT 01-MAY-2000 (TRMSBLrel. 13, Last sequence update:
 DT 01-OCT-2002 (TRMSBLrel. 22, Last annotation update:
 DE Vxo-inositol hexaphosphate phosphohydrolase precursor
 (EC 3.1.3.8).
 LE Aspergillus niger.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiaceae; Trichocomaceae; Mitosporic trichocomaceae; Aspergillus.
 CX NCBI_TaxID=5061;
 RN 1.
 PP SEQUENCE FROM N.A.
 PA Hongming W., Qi W., Jing X.:
 "PCR cloning and characterization of the phytase (phyA) gene of
 Aspergillus niger (China Strain)".
 R1 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DP EXBL; AF218813; AAF25461.1;
 DR HSSP; F34752; 11HP.
 DR InterPro; IPR000563; HisAc phsphtse.
 DE Pfam; PF03328; acid phosphat.
 DR PROSITE; PS00616; HIS-ACID-PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS-ACID-PHOSPHAT_2; 1.
 KW Hydrolyase; Lyase; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 SQ SEQUENCE 467 AA; 51030 MW; F4300A8F165BF92 CRC64;

Query Match 98.3%; Score 2294; DB 3; Length 467;

Best Local Similarity 97.5%; Pred. No. 1.9e-167;

Matches 433; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASRNSQSDTVQGYQCFSESHLWQYAPFFSLANESVISPEVAGCRVTFQVLSRHG 60

Db 24 ASRNSQSDTVQGYQCFSESHLWQYAPFFSLANESVISPEVAGCRVTFQVLSRHG 83

Cy 61 ARYPTDSKKYSALITEEQGNATTFDGYAFKTYNYSLGADDTPTFGEQLVNSGKIF 120

```

DB 84 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVSGIKF 143
QY 121 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 144 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 240
DB 204 SSSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 263
QY 241 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPAFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNSATFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 383
QY 361 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 420
DB 384 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 443
QY 421 CTRDSFVRGLSPARSGGDWAECEFA 444
DB 444 CTRDSFVRGLSPARSGGDWAECEFA 467

RESULT 2
ID Q8255 PRELIMINARY: PRT: 448 AA.
AC Q8255:
DT 01-MAR-2003 (Tremblre): 23, Created:
DT 01-MAR-2003 (Tremblre): 23, Last sequence update:
DE Phycase (fragment).
GN PHVA.
OS Aspergillus ficium.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5098;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Zhu J., Xu Z., Wang L., Chen G., Jiang H., Li X.:
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF57344; AN10115.1;
FT NON-TER
SQ SEQUENCE 448 AA; 49260 MW; 0554FF9712FF7BAA CRC64;

Query Match 96.8%; Score 2260; DB 3; Length 448;
Best Local Similarity 95.5%; Pred. No. 7.4e-165;
Matches 424; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 ASRNSGSDTVQGYQCFSETSHLWQYAPFFSLANKSAISPDVPAQCQVFAQVLSRHG 60
DB 5 ASRNSGSDTVQGYQCFSETSHLWQYAPFFSLANKSAISPDVPAQCQVFAQVLSRHG 64
QY 61 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVSGIKF 120
DB 65 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVSGIKF 124
QY 121 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 125 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 184
QY 181 SSSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 240
DB 185 STSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 244
QY 241 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 245 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 304
QY 301 IARLTHSPVHDDTSSNHTLDSSPAFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360

```

```

DB 305 IARLTHSPVHDDTSSNHTLDSSPAFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 364
QY 361 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 420
DB 365 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 424
QY 421 CTRDSFVRGLSPARSGGDWAECEFA 444
DB 425 CTRDSFVRGLSPARSGGDWAECEFA 448

RESULT 3
ID C93838 PRELIMINARY: PRT: 467 AA.
AC C93838:
DT 01-MAY-1999 (Tremblre): 10, Created:
DT 01-MAY-1999 (Tremblre): 10, Last sequence update:
DT 01-JUN-2002 (Tremblre): 21, Last annotation update:
DE Phytase.
GN PHVA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes.
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.:
RL "Phytase having high-affinity for phytic acid."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases
DR EMBL: AB22700; BAA74433.1;
DR HSP: P34752; IHP.
DR InterPro: IPR003560; HisAc_phosphatase.
DR Pfam: PFO328; acid_phosphat; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51028 MW; 7A38ED543EDC265C CRC64;

Query Match 96.8%; Score 2259; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 9.4e-165;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASRNSGSDTVQGYQCFSETSHLWQYAPFFSLANKSAISPDVPAQCQVFAQVLSRHG 60
DB 24 ASRNSGSDTVQGYQCFSETSHLWQYAPFFSLANKSAISPDVPAQCQVFAQVLSRHG 63
QY 61 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVSGIKF 120
DB 84 ARYPTDSKGGKYSALIEEIQQWATTFDCKYAFELKTYNYSJGADDLTPFGECELVSGIKF 143
QY 121 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 180
DB 144 YORYESLNRNVPFIRSSGSSRVIASGKKFEGFQSTKLKOPRAQPGQSSPKIDWVISEA 203
QY 181 SSSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 240
DB 204 STSNNTLDPGCTVFEDESELADTVEANTATVPFSIRORLNDLSCVTLTDTVTYLYMD 263
QY 241 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSFCDLFTHEWKNYDYQSLKKYVGHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDDTSSNHTLDSSPAFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 324 IARLTHSPVHDDTSSNHTLDSNPATFLPNSTLYADFSDHNGIISILFALGLYNGTKPLST 363
QY 361 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 420
DB 384 TTVENITQDGFSSANTVPFASRLYVEMMQCAEQEPVRLVNDRVVPLHGCPVDALGR 443
QY 421 CTRDSFVRGLSPARSGGDWAECEFA 444

```



```
DB 444 CTRDSFVXGJSPARSGDNGECFA 467
RESULT 4
Q9HEQ0 PRELIMINARY; PRT: 467 AA.
AC Q9HEQ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phytase
OS Aspergillus fumigatus
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
OX NCBI_TaxID=5058;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang J., An L., Wang Y., Yuan X.;
RJ Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013315; AAG40885.1;
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000550; HisAc_phosphatase.
DR Pfam; PF03328; acid_phosphatase_1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B8565E CRC64;
Query Match 96.4%; Score 2249; DB 3; Length 467;
Best Local Similarity 95.3%; Pred. No. 5.5e-164;
Matches 423; Conservative 14; Mismatches 7; Indels 0; Gaps 0;
QY 1 ASRQSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVLSRHG 60
DB 24 ASRQSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVLSRHG 63
QY 61 ARYPDSKGGKYSALIEEIQONATTEDGKYAFKTYNSLGGADLTTPGEQELVNSGKIF 120
DB 84 ARYPDSKGGKYSALIEEIQONATTEDGKYAFKTYNSLGGADLTTPGEQELVNSGKIF 143
QY 121 YQRYESLTRNIVPPIRSSGSSRVASGKKFIEGFQSTKLKOPRAQPGQSSPKIDVWISAE 180
DB 144 YQRYESLTRNIVPPIRSSGSSRVASGKKFIEGFQSTKLKOPRAQPGQSSPKIDVWISAE 203
QY 181 SSNNLTDSGCTVDFSELAQDIEANFTATFVPSIRQLENLDSGVSLTCTEVTYLMDM 240
DB 204 SSNNLTDSGCTVDFSELAQDIEANFTATFVPSIRQLENLDSGVSLTCTEVTYLMDM 263
QY 241 CSFDTISTSTVDTKLSPPFCDFTHDEKWNQYVLSLKKYVGHGAGNPLGPTQGVYANEL 300
DB 264 CSFDTISTSTVDTKLSPPFCDFTHDEKWNQYVLSLKKYVGHGAGNPLGPTQGVYANEL 323
QY 301 IARLTHSPVHDTSNHTTLOSSPATFPLNSTLYADFSHDNGIISILFALGLVNGTKPLST 360
DB 324 IARLTHSPVHDTSNHTTLOSSPATFPLNSTLYADFSHDNGIISILFALGLVNGTKPLST 383
QY 361 TTVENITQDGFSSAMTVFASRLVEMMQCCAEQEPVRYLVNDRVYPLHCCPVDALGR 420
DB 384 TTVENITQDGFSSAMTVFASRLVEMMQCCAEQEPVRYLVNDRVYPLHCCPVDALGR 443
QY 421 CTRDSFVXGJSPARSGDNGECFA 444
DB 444 CTRDSFVXGJSPARSGDNGECFA 467
RESULT 5
Q9CIT1 PRELIMINARY; PRT: 466 AA.
AC Q9CIT1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phytase.
OS Aspergillus fumigatus (Sartorya fumigata)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
OX NCBI_TaxID=5058;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.
RA STRAIN=ATCC 34625;
RX MEDLINE=97288C63; PubMed=9143104;
```

RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
RT "Gene cloning, purification, and characterization of a heat-stable
R1 phytase from the fungus *Aspergillus fumigatus*.";
R2 Appl. Environ. Microbiol. 63:1696-1700(1997).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H2O = D-MYO-
CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
CC A pH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A pH RANGE OF 2.5 TO
CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
CC CELSIUS OVER A PERIOD OF 20 MIN. WITH A LOSS OF ONLY 10% OF THE
CC INITIAL ENZYMIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL: U59804; AAB96872.1; -;
DR HSSP: P34752; 11RP.
DR InterPro: IPR000560; HisAc_phsphtase.
DR Pfam: PF03128; acid_phosphat_1;
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1;
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1;
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 26
FT CHAIN 27 465 3-PHYTASE A.
FT ACT_SITE 81 91 REQUIRED FOR BINDING SUBSTRATE
(BY SIMILARITY).
FT ACT_SITE 82 92 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 359 359 PROTON DONOR (BY SIMILARITY).
FT DISULFID 30 39 BY SIMILARITY.
FT DISULFID 73 412 BY SIMILARITY.
FT DISULFID 213 463 BY SIMILARITY.
FT DISULFID 262 280 BY SIMILARITY.
FT DISULFID 434 442 BY SIMILARITY.
FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;

Query Match 68.8%; Score 1605.5; DB 3; Length 465;
Best Local Similarity 66.4%; Pred. No. 9,4e-115;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 1 ASRQSCDTVDGQYQCFSETSHLWQYAPFFSLANESVISPEVPAQGRVTFACVLSRHGA 61
DB 1 SAGSKSCDTVDLGYQCSPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGA 60
QY 61 RYPTDSKGGKYSALIEEIQONATFDGKYAPKTYNYSLGACDLTPGEQELVNSGKIFY 120
DB 23 SAGSKSCDTVDLGYQCSPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGA 82
QY 61 RYPTDSKGGKYSALIEEIQONATFDGKYAPKTYNYSLGACDLTPGEQELVNSGKIFY 120
DB 83 ARYPTSSKKYKKLVTAICANATDFKGPATKTYNYTLGADCLTPGEQELVNSGKIFY 142
QY 121 QRYESLFRNIVPFRSSGSRVIAAGKPFEGFQSTKCKPRAQPCSSPKIDVISEAS 180
DB 143 QRYKALARSVVVPRASSGSRVIAAGKPFEGFQCAKADPGA-TNRAAPALSVIPESE 201
QY 181 SSNNLTDPGCTVFESSELAQTVANFTATFVPSIRQLENDLSGVTLTTEVTVLMDM 240
DB 202 EFNNTLDHGVCCTKFEASQIGDEVAANFTALFAPDIRARAEKHLPGVTLTDECVSLMDV 261
QY 241 CSFDTISTSTVDTKLSPFCDLFDHDKINVDYLSLKKYVGHGAGNP-GPTCGVGVANELI 300
DB 262 CSFDTVARTSDASQSPFCQLFTHNWKKNYVLSLGGYVGHGAGNP-GPTCGVGVANELI 321
QY 301 IARLTHSPVHDTSSNHTLDSSPATFPJNSTLYADFSDHNGIISILFALGLYNGTKPLST 360
DB 322 IARLTRSPVQDHTSTNSTLVSNPATFPJNATMYVDFSDHNSMWSIFFALGLYNGTEPLSR 381
QY 361 TVENITQDGFSSAWTVFFASRLYVEMVQCAQEFPLRVLVNDRVPLHGCVDALGRC 420
DB 382 TSVESAKELDGYASVWVPPFGARAYFETMCKSEKEPLVRALINDRVVPLHGCVDKLGRC 441

QY 421 CTSDSFVRGLSFARSGGDWAECPA 444
DB 442 CKLNDPVGKLSWARSNGNMGECFS 465

RESULT 7
ID Q8WZJ5 PRELIMINARY; PRI: 442 AA.
AC Q8WZJ5;
DT 01-VAR-2002 (T-EMBLrel. 20, Created;
DT 01-VAR-2002 (T-EMBLrel. 20, Last sequence update;
DT 01-VAR-2003 (T-EMBLrel. 23, Last annotation update;
DE Pyrtase (EC 3.1.3.8) precursor (fragment).
GN PHA3.
OS *Aspergillus fumigatus* (Sartorya fumigatus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
QX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCICC AF93024;
RA Zhang G.;
RT "Cloning of phytase gene from *Aspergillus fumigatus* and its expression
in *Pichia pastoris*.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ419776; CAC12529.1; -;
DR InterPro: IPR000560; HisAc_phsphtase.
DR Pfam: PF00328; acid_phosphat_1;
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1;
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1;
KW Signal; Hydrolase.
FT SIGNAL 1 1
FT CHAIN 41 442 POTENTIAL.
FT SIGNAL 41 442 PHYTASE.
SQ SEQUENCE 442 AA; 48485 MW; 3FDBAC656A268514 CRC64;

Query Match 68.8%; Score 1605.5; DB 3; Length 442;
Best Local Similarity 66.4%; Pred. No. 1e-114;
Matches 295; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 2 SRQSSCOTVDGQYQCFSETSHLWQYAPFFSLANESVISPEVPAQGRVTFACVLSRHGA 61
DB 1 SAGSKSCDTVDLGYQCSPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGA 60
QY 62 RYPTDSKGGKYSALIEEIQONATFDGKYAPKTYNYSLGACDLTPGEQELVNSGKIFY 121
DB 61 RYPTSSKKYKKLVTAICANATDFKGPATKTYNYTLGADCLTPGEQELVNSGKIFY 120
QY 122 QRYESLFRNIVPFRSSGSRVIAAGKPFEGFQSTKCKPRAQPCSSPKIDVISEAS 181
DB 121 QRYKALARSVVVPRASSGSRVIAAGKPFEGFQCAKADPGA-TNRAAPALSVIPESE 179
QY 182 SSNNLTDPGCTVFESSELAQTVANFTATFVPSIRQLENDLSGVTLTTEVTVLMDM 241
DB 180 TENNTLDHGVCCTKFEASQIGDEVAANFTALFAPDIRARAEKHLPGVTLTDECVSLMDM 239
QY 242 SFDTISTSTVDTKLSPFCDLFDHDKINVDYLSLKKYVGHGAGNP-GPTCGVGVANELI 301
DB 240 SFDTVARTSDASQSPFCQLFTHNWKKNYVLSLGGYVGHGAGNP-GPTCGVGVANELI 299
QY 302 IARLTHSPVHDTSSNHTLDSSPATFPJNSTLYADFSDHNGIISILFALGLYNGTKPLST 361
DB 300 ARLTRSPVQDHTSTNSTLVSNPATFPJNATMYVDFSDHNSMWSIFFALGLYNGTEPLSR 359
QY 362 TVENITQDGFSSAWTVFFASRLYVEMVQCAQEFPLRVLVNDRVPLHGCVDALGRC 421
DB 360 SVESAKELDGYASVWVPPFGARAYFETMCKSEKEPLVRALINDRVVPLHGCVDKLGRC 419
QY 422 TRDSFVRGLSFARSGGDWAECPA 444
DB 420 KLANDPVGKLSWARSNGNMGECFS 442

RESULT 8
 CC0100 PRELIMINARY: PRT: 466 AA.
 ID C00100
 AC C00100
 CT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update:
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update:
 DE 3-phosphate precursor (EC 3.1.3.8) (MYO-inositol hexakisphosphate
 DE phosphohydrolase) (3 phosphate) (MYO-inositol hexakisphosphate
 DE phosphohydrolase)
 DE Aspergillus terreus.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
 CX NCBI_taxid=33178;
 RN (1)
 RN SEQUENCE FROM N.A.
 RC STRAIN=CBS 116.46;
 RA Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B.,
 RA Broser C., van Loon A.P.;
 RA Submitted (JUN-1996) to the EMBL/GenBank/DBS databases.
 CC - FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE (BY SIMILARITY).
 CC - CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H2O = D-MYO-
 INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC - SUBCELLULAR LOCATION: SECRETED.
 CC - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CR EMBL: J60412; AAB58485.1; -
 CR HSP: P34752; LIHP.
 CR InterPro: IPR000560; HisAc_phosphatase.
 DR Pfam: PF00328; acid_phosphat_1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolyase; Glycoprotein; Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 466 3-PHOSPHATASE.
 FT ACT_SITE 92 92 REQUIRED FOR BINDING SUBSTRATE
 (BY SIMILARITY).
 FT ACT_SITE 83 93 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT D1SULFID 31 40 BY SIMILARITY.
 FT D2SULFID 71 414 BY SIMILARITY.
 FT D3SULFID 215 465 BY SIMILARITY.
 FT D4SULFID 264 282 BY SIMILARITY.
 FT D5SULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 105 135 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC... (POTENTIAL).
 SQ SEQUENCE 466 AA; 51055 MW; F2ABCECAAF7C22C4 CRC64;
 Query Match 65.1%; Score 1520; DB 3; Length 466;
 Best Local Similarity 61.4%; Pred. No. 4e-106;
 Matches 279; Conservative 65; Mismatches 96; Indels 0; Gaps 0;
 QY 4 NOSSCCTVDGQYCFSETSHLMGQYAPFFSLANESVISPEVAGGCVTFAQVLSHGRARY 63
 DB 27 NNSDCTSVDRGVOCYFELSHKGLYAPFSLJCESPFELVDVDCCHI:FFQVLAHGRAS 86
 QY 64 PTDSKGGKYSALJEETQOATTFDGGYALFKYNYSLGACDLTPFGDEELVNSG:KFKYCR 123
 DB 87 PTDSKTKAVAAATTAALQKATALPGKYAFJCKSYNYSMSSENLPFGNQLDGLGACFYRR 146
 QY 124 YESLIRNIVPEFRSSGSRVIAAGKFFIGFSTK:KOPRAOPGOSSPKIDVWSEASSS 183
 DB 147 YDLTRHINPFRVRAAUSRRHSEAKFVGGFQVARGGDPHAPHGFSFRAVDVWIFEGTAY 206
 QY 184 NNTLCFGCTCTVFEDSELADTVSEANFTATVPVSIROIRLENDLSGVLTDTEVTYLMCGSF 243

DR Pfam: PF03028; acid phosphatase; 1.
 DR PROSITE: PSC616; HIS-ACID-PROSPHAT_1; 1.
 DR PROSITE: PS00778; HIS-ACID-PROSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN 2 487 3-PHYTASE A.
 FT DOMAIN 267 270 POU-SER.
 FT DOMAIN 423 433 POLY-GLY.
 FT ACT_SITE 75 75 REQUIRED FOR BINDING SUBSTRATE
 FT ACT_SITE 75 75 (BY SIMILARITY).
 FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 362 368 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 26 35 BY SIMILARITY.
 FT DISULFID 64 421 BY SIMILARITY.
 FT DISULFID 208 485 BY SIMILARITY.
 FT DISULFID 260 289 BY SIMILARITY.
 FT DISULFID 456 464 BY SIMILARITY.
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 487 AA; 52537 MW; 97310EDC83D051DB CRC64;

Query Match 48.4%; Score 1129.5; DB 3; Length 487;
 Best Local Similarity 45.8%; Pred. No. 3.6e-78;
 Matches 217; Conservative 73; Mismatches 145; Indels 29; Gaps 4;

OY 8 CDTVDGQYQCFSETSHLMGQYAPFFSLANESVISPVAGCRVTFACVLSRHGARYPTDS 67
 DB 26 CDTPLGFCQGTAFSHFGQVSPVSE--LDASIPDCCEVTFACVLSRHGARYPTLX 83
 OY 68 KKKYSAIIEICQNAITTFQSKYAFKTYNYSLGADLTPFGDELVNSGKIFYRFS 127
 DB 54 RAASVYDLDRHHGAISYGGYEFRTYDYVTLGADLTITGQQQMNWSGKIFYRYRAL 143
 OY 128 TRNIVPFRSSGSSRVIASGKKFIEGFQSTKLKDPRAQFGOSSPKIDVVISGSSNNTL 187
 DB 144 ARKSIPFVATAGQDRVISAENFTGQFHSALLADRGSTVPTPLFDVNVVIVETAGANNIL 203
 OY 188 DRGTCVPE--SELADTVEANFTATFVESIRQRIENDLSGV--TDTETVYVXDMCSFD 244
 DB 204 HNDLCTAREEGPYSTIGDCAQDTLSTAGPITARVNAKIPCANITDADTVALNCLQPER 263
 OY 245 TSTSTVD-----TKSPFCDFTHDEW--NYDYLSLKKYVGHGAGNPLGPTQG 293
 DB 264 TVASSSSDPATADAGGNGRPLSPFCRUFSESEMAAYDYLSVSGWYGYGFGNPLGPTQG 323
 OY 294 VQYANELARLTHSPVHDTSSNHTLDSPATFPLKSTLYADFSDHNGIISLPLALGLYN 353
 DB 324 VQVVELLARLAGVPRDGTSTNRTLDGPRFPLGRFLYADFSDHNDMNGVHLGALGAYD 383
 OY 354 GTPKSTTTVENITQDGFSSAWTVPFASRLVYEMMQC-----QAEQEPPLVR 400
 DB 384 GVPPDKTARROPPEELGGVAASNAVPPAARIIVKXNRSGSGGGGGGGGGEQKQEMVR 443
 OY 401 VLVNDRVPLHCPVDALGRC--RDSFVRLSLFARSQGWAECPA 444
 DB 444 VLVNDRVMTLKGCGADERGCMCTLERFIESAFARGNGKWDLCFA 487

RESULT 12
 Q96VF5 ID Q96VF5 PRELIMINARY; PRT; 443 AA.
 AC Q96VF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase precursor (EC 3.1.3.26).
 GN PHYA.
 OS Trametes pubescens.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=154538;

11.
 SEQUENCE FROM N.A.
 RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
 RA Wyss M., Fuglsang C.C.;
 RT "Expression cloning and characterization of five novel phytases from
 RT four basidiomycete fungi; Peniophora lycii, Agrocybe pediades, cf.
 RT Ceriophora and Trametes pubescens";
 RL Submitted (MAR-2001) to the EMBL/GenBank/CCBJ databases.
 DR EMBL; AJ310700; CAC48234.1; .
 DR InterPro: IPR000563; HisAc_Phsptase.
 DR Pfam: PF03028; acid phosphatase; 1.
 DR PROSITE: PS00656; HIS-ACID-PROSPHAT_1; .
 DR PROSITE: PS00778; HIS-ACID-PROSPHAT_2; .
 KW Hydrolase; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 443 PHYTASE.
 SQ SEQUENCE 443 AA; 47773 MW; 13D4BEC0B049D1 CRC64;

Query Match 32.7%; Score 762.5; DB 3; Length 443;
 Best Local Similarity 39.0%; Pred. No. 4.2e-50;
 Matches 174; Conservative 70; Mismatches 167; Indels 35; Gaps 12;

OY 3 RNOSCDTVGQYQCFSETSHLMGQYAPFFSLANESVISPVAGCRVTFACVLSRHGAR 62
 DB 28 RDTSACLDTRDVQ-----QSMWSPYFPAA--TVVAP--PASCINQVH--QRHGR 77
 OY 63 YPTDSKGGKYSALIEICQNAITTFQSKYAFKTYNYSLGADLTPFGDELVNSGKIFYQ 122
 DB 78 FPTSGAARKIQTAVAKLKAASNTDPLAFVNTYSLGQCSLVELGATQSSSAGQEAFT 137
 OY 123 RYESL--TRNIVPFRSSGSSRVIASGKKFIEGFQSTKLKDPRAQFGOSSPKIDVVISAS 181
 DB 136 RYSSLVADEPPFVAGSDRVVATANNWTAGF-----ALASSNTTPVLSVISEA- 189
 OY 182 SSNTLDPGTCVFESELAADTVEANFTATFVESIRQRIENDLSGVTLTDTETVYVXDMC 241
 DB 190 -GNDTLDDNMCPAAGDS---DPQVQMLAQFAPPMTARLNAGAPGANLTDTDTYNLLTL 245
 OY 242 SPTISTSTVTKLSPFCDFTHDEW--NYDYLSLKKYVGHGAGNPLGPTQGVYANEL 350
 DB 246 PFETVATE---RRSEPCDYEELQAECAFAYKADLKPYGTYGQFGVGVGVYVNEL 351
 OY 301 EASLTHSPVHDTSSNHTLDSPATFPLKSTLYADFSDHNGIISILFALGLYNTRPLST 360
 DB 302 EASLTHSPVHDTSSNHTLDSPATFPLKSTLYADFSDHNGIISILFALGLYNTRPLST 361
 OY 361 TTVENITQDGFSSAWTVPFASRLVYEMMQCQAEQEPPLVYVNDRVVPLHGPCVDALGP 420
 DB 362 TTPD---PASTELVKKIVPFSARMVVERLDCGGAQS--VALYKNDACVCLAPCGASTSGV 416
 OY 421 CTRDSFVRLSLFARSQ--QSWAECPA 444
 DB 417 CLTDAFVESQAYARNDEGDFEKCPA 442

RESULT 13
 Q96VF5 ID Q96VF5 PRELIMINARY; PRT; 439 AA.
 AC Q96VF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Phytase precursor (EC 3.1.3.26).
 GN PHYA.
 OS Peniophora lycii.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Jaccmocladiaceae; Peniophora.
 OX NCBI_TaxID=154539;
 11.
 SEQUENCE FROM N.A.
 RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
 RA Wyss M., Fuglsang C.C.;
 RT "Expression cloning and characterization of five novel phytases from

RT four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, cf.
 RT Ceriporia and Trametes pubescens";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBAJ databases.

DR EMBL: AJ310696; CAC48195.1;
 DR InterPro: IPR003560; HisAc_phsphtse.

DR Pfam: PF00328; acid_phosphat;
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.

DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Signal.

FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 439 PHYTASE.

SQ SEQUENCE 439 AA; 47563 MW; F668FA9D3839DDA CRC64;

Query Match 32.2%; Score 752.5; DB 3; Length 439;
 Best Local Similarity 40.5%; Pred. No. 2.4e-49;
 Matches 175; Conservative 53; Mismatches 151; Indels 53; Gaps 15;

QY 25 WGOYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGGKYSALIEEIQONAT 84

DB 41 WGYDPFFPV--EPAAP--PEGCTVTQVNLQRHGARKPTSGARSQVAVAKIQVAP 96

QY 85 TFDGKYAFKTNYSLGADLLTPFGQELVNSGIKFYORYESL-TRNTVPFIRSSGSSRV 143

DB 97 FTDPKYEFNLDPVYKFGVADLLPFGANQSHQTGTXYTRYSTLFEGGDVPFVRAAGGRV 156

QY 144 ASGKKF-EGFOSKLDKOPRAGQSS-----PKIDVVISSEASSNNLTDPGCTCTVFED- 197

DB 157 VDSSTNWTAGF-----GASGETVLTQVQLQE-----EGNCTLCNM 195

QY 198 --SELACTVEANFTATFVSIRQRLNDSGLVTLTDTVTYLMDCSPDTISTSTVDTKL 255

DB 196 CPNEVDGDESTWLGVPAPNITARLNAAPSANLSDSALTLMDMCPFDTLSSGNA--- 251

QY 256 SPFCOLFTHDEWINDYLSKKYGHGAGNPLGPTQGVYANELIARLTHSPVHDTSS 315

DB 252 SPFCOLFTAEYSVSEYVYDLYKTYGTGPGNALGPVQGVYVNEALLRATGAVRDETQT 311

QY 316 NHTLSSPATFTLNLTVACDFSHNGIISILFALGLYNGT--KP-STTTVENITOTDGS 373

DB 312 NHTLSDSPATFTLNLTVACDFSHNTMPVIFALGLFNATALDPAKPD--ENRIAVD--- 366

QY 374 SAWTVPFASRLYVEMMQCAECPVRLVNDRVVPLHGC-PVDALGRCRTDSSFVRGLSF 432

DB 367 -SKLVPPFSGHNTVEKLACSGKE-AVRVLNDAVQPLFECGGVD--GYCE-SAFVESQTY 421

QY 433 ARSG--GDWAC 442

DB 422 ARENGCGGFAK 433

RESULT 14

Q96VTC

ID Q96VTC PRELIMINARY; PRT; 453 AA.

AC Q96VTC

DT 01-DEC-2001 (TrEMBLrel. 19, Created;

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update;

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Phytase precursor (EC 3.1.1.26).

GN PHA.

OS Agrocybe pediades.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Agaricales; Boletiales; Agrocybe.

OX NCBI_TaxID=84607;

RN [1]

RP SEQUENCE FROM N.A.

RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,

RA Wyss M., Fuglsang C.C.;

RT "Expression cloning and characterization of five novel phytases from

RT four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, cf.

RT Ceriporia and Trametes pubescens.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBAJ databases.

DR EMBL: AJ310697; CAC48160.1;

DR InterPro: IPR000560; HisAc_phsphtse.

DR Pfam: PF00328; acid_phosphat; 1.

DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.

KW Hydrolase; Signal.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 453 PHYTASE.

SQ SEQUENCE 453 AA; 49931 MW; D62FIAEFA1091E5D CPC64;

Query Match 31.7%; Score 739.5; DB 3; Length 453;

Best Local Similarity 36.8%; Pred. No. 2.5e-48;

Matches 161; Conservative 83; Mismatches 152; Indels 41; Gaps 11;

QY 25 WGOYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGGKYSALIEEIQONAT 84

DB 39 WAAATPYYPV--QAYTPP--PKDCKTQVNIQRHGARFTSGAGTRIQAAYKKJCSAKT 94

QY 85 TFDGKYAFKTNYSLGADLLTPFGQELVNSGIKFYORYESL-TRNTVPFIRSSGSSRV 143

DB 95 YTDPRDLFTNVTYTLGHDDLVPFGALQSSQAGEETFORYSFLVSKENLPFYRASSNRV 154

QY 144 IASGKXFEIGFOSKLDKOPRAGQSSPKIDVVISSEASSNNLTDPGCTCTVFEDSELADT 203

DB 155 VDSATNWTGESA-----ASHVNLNPLFVLSE--SLNDTECDAMC---PNAGSSDP 202

QY 204 VEANFTATFVPSIRQRLNDSGLVTLTDTVTYLMDCSFDTISTSTVDTKLSPPCDLFT 263

DB 203 QGIVTSITVGTPIANRLNQAPGANITADVNLPPLCAFEIIVKETP-----SPFCNLT 258

QY 264 HDWINDYLSKKYGHGAGNPLGPTQGVYANELIARLTHSPVHDTSSNHTLDSRP 323

DB 259 PEEFAQFEVGLDKFYGTGYGQPLGPVQGVYINELLARLTMPVRDNTQNRITLDSRP 318

QY 324 ATPPLNSTLYADESHONGIISILFALGLYNGTKPLSTTTVENITQDGFSSAKTVFASR 383

DB 319 LTPPLORSIYADLSHONQIATFSAMGLFNQSPLD-PFPPNPKRT--WTSRLTDFSR 375

QY 384 LYVEMMQCAE-----QEPVRLVNDRVVPLHGCPEVDALGRCRTDSSPVR 428

DB 376 WYTERLQGEDGTGSGSPSRIMRNGNVQTFVRLVNDALQPLKFCGGMDSCTLEAFVE 435

QY 429 GLSFARSG--GDWAC 443

DB 436 SKYAREDDGGDFEXCF 452

RESULT 15

Q96VK9

ID Q96VK9 PRELIMINARY; PRT; 442 AA.

AC Q96VK9

DT 01-DEC-2001 (TrEMBLrel. 19, Created;

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Phytase precursor (EC 3.1.1.26).

GN PHA.

OS Ceriporia sp. CBS 100231.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Agaricales; Ceriporia.

OC NCBI_TaxID=154783;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CBS 100231.

RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,

RA Wyss M., Fuglsang C.C.;

RT "Expression cloning and characterization of five novel phytases from

RT four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, cf.

RT Ceriporia and Trametes pubescens.";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBAJ databases.

DR EMBL: AJ310698; CAC48163.1;

DR InterPro: IPR000560; HisAc_phsphtse.

DR Pfam: PF00328; acid_phosphat; 1.

DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.

DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.

KW Hydrolase; Signal.

```

FT SIGNAL      1 19      PTENTIAL.
FT CHAIN       20 442    PHYTASE.
SQ SEQUENCE    442 AA; 47915 MW; 0464C1C691D86702 CRC64;

Query Match      31.7%; Score 139; DB 3; Length 442;
Best Local Similarity 41.0%; Pred. No. 2.6e-48;
Matches 175; Conservative 64; Mismatches 154; Indels 34; Gaps 14;

Qy 25 WGOYAPFFSLANESVISFEVPAGCRVTFQAQVLSRHGARYPTDSKGGKYSALIEEIQ-QN 82
Db 40 WSPYSPYFPCEAEYKA----PPAGCINQVNIIOPHGARFPTSGATTIRKAGLTKLGVQN 95
Cy 53 ATTEGKYAFKTYNYSLGADDLTPGCEQLVNSGKIFYORYESL-TRNIVPPIRSSGSS 141
Db 96 FT--DAKFNTIKSKYFLGNSDLVPFGAAGSFDAGQEAFAFYKLYSKNLPFIRADGSD 153
Cy 142 RVIASGKKFIEGFOSTKLDPPRAQPGOSSPKIDVWISSESSNNLTLPDGTCTVFEDSELA 201
Db 154 RVVDSATNWTAGFAS-----ASHNTVQPKLNLIIPQ--TGNDTLEDNMCPAAGSD-- 202
Cy 202 DTVEANFTATVPPIRORJENDLSGVTLTDTETVYLMCMSEDTCTSTVTVTKLSFFCDL 261
Db 203 PQVNAWLAVAP-PSITARLAAAPSVNLTDTDAFNLSLCAFLTVSKE----KKSDFTL 257
Cy 262 F--THDEWINVDYLSLKKYXGHCAGNPLGPTCGGVYANEELIARLTHSPVHDDTSSNHTL 319
Db 258 FEGIPGSFEAFAYGGDLKDFYGTGYGELGVQGVYNEELIARLTKSAVRENTQNRLL 317
Cy 320 DSSPATPPKASTLYADFSHONGIISILFALGLVNGTKPLSTTTVENITQTDGFSSAMTVP 379
Db 318 DASPVTPPLNKTFFYADFSHCNLMYAVFSAXGLFQAPPLS-CSVNPNWRTMTSS--LXP 374
Cy 380 FASRLYVEMKCCQAEQEPVAVVJNDRVVPLHGCVPDAJGRCTRDSFVRGLSPARS--GG 437
Db 375 FSGRMVVERLSGFGTTK--VAVLVQDVQVPLEFCGGRNGLCTLAKEVESCTPARSDGAG 432
Cy 438 DWAECEFA 444
Db 433 DFEKCEFA 439

```

Search completed: November 12, 2003, 14:32:48
 Cdb time : 41 secs